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|              |    |        |  |
|--------------|----|--------|--|
| NEWS         | 1  |        | Web Page URLs for STN Seminar Schedule - N. America  |
| NEWS         | 2  |        | "Ask CAS" for self-help around the clock   |
| NEWS         | 3  | SEP 09 | CA/CAPLUS records now contain indexing from 1907 to the present  |
| NEWS         | 4  | DEC 08 | INPADOC: Legal Status data reloaded  |
| NEWS         | 5  | SEP 29 | DISSABS now available on STN   |
| NEWS         | 6  | OCT 10 | PCTFULL: Two new display fields added  |
| NEWS         | 7  | OCT 21 | BIOSIS file reloaded and enhanced  |
| NEWS         | 8  | OCT 28 | BIOSIS file segment of TOXCENTER reloaded and enhanced   |
| NEWS         | 9  | NOV 24 | MSDS-CCOHS file reloaded   |
| NEWS         | 10 | DEC 08 | CABA reloaded with left truncation   |
| NEWS         | 11 | DEC 08 | IMS file names changed   |
| NEWS         | 12 | DEC 09 | Experimental property data collected by CAS now available in REGISTRY  |
| NEWS         | 13 | DEC 09 | STN Entry Date available for display in REGISTRY and CA/CAPLUS   |
| NEWS         | 14 | DEC 17 | DGENE: Two new display fields added  |
| NEWS         | 15 | DEC 18 | BIOTECHNO no longer updated  |
| NEWS         | 16 | DEC 19 | CROPU no longer updated; subscriber discount no longer available   |
| NEWS         | 17 | DEC 22 | Additional INPI reactions and pre-1907 documents added to CAS databases  |
| NEWS         | 18 | DEC 22 | IFIPAT/IFIUDB/IFICDB reloaded with new data and search fields  |
| NEWS         | 19 | DEC 22 | ABI-INFORM now available on STN  |
| NEWS         | 20 | JAN 27 | Source of Registration (SR) information in REGISTRY updated and searchable   |
| NEWS         | 21 | JAN 27 | A new search aid, the Company Name Thesaurus, available in CA/CAPLUS   |
| NEWS         | 22 | FEB 05 | German (DE) application and patent publication number format changes   |
| NEWS         | 23 | MAR 03 | MEDLINE and LMEDLINE reloaded  |
| NEWS         | 24 | MAR 03 | MEDLINE file segment of TOXCENTER reloaded   |
| NEWS         | 25 | MAR 03 | FRANCEPAT now available on STN   |
| NEWS         | 26 | MAR 29 | Pharmaceutical Substances (PS) now available on STN  |
| NEWS         | 27 | MAR 29 | WPIFV now available on STN   |
| NEWS         | 28 | MAR 29 | No connect hour charges in WPIFV until May 1, 2004   |
| NEWS         | 29 | MAR 29 | New monthly current-awareness alert (SDI) frequency in RAPRA   |
| NEWS EXPRESS |    |        | MARCH 5 CURRENT WINDOWS VERSION IS V7.00A, CURRENT MACINTOSH VERSION IS V6.0b(ENG) AND V6.0Jb(JP), AND CURRENT DISCOVER FILE IS DATED 3 MARCH 2004 |
| NEWS HOURS   |    |        | STN Operating Hours Plus Help Desk Availability  |
| NEWS INTER   |    |        | General Internet Information   |
| NEWS LOGIN   |    |        | Welcome Banner and News Items  |
| NEWS PHONE   |    |        | Direct Dial and Telecommunication Network Access to STN  |
| NEWS WWW     |    |        | CAS World Wide Web Site (general information)  |

Enter NEWS followed by the item number or name to see news on that specific topic.

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\* \* \* \* \* STN Columbus \* \* \* \* \*

FILE 'HOME' ENTERED AT 17:55:13 ON 29 MAR 2004

|   |            |         |
|---|------------|---------|
| => file medline, uspatful, dgene, embase, wpids, fsta, cen, biosis, |            |         |
| COST IN U.S. DOLLARS  | SINCE FILE | TOTAL   |
|   | ENTRY      | SESSION |
| FULL ESTIMATED COST   | 0.21       | 0.21    |

FILE 'MEDLINE' ENTERED AT 17:55:41 ON 29 MAR 2004

FILE 'USPATFULL' ENTERED AT 17:55:41 ON 29 MAR 2004  
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FILE 'BIOSIS' ENTERED AT 17:55:41 ON 29 MAR 2004  
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=> s FRT/FLP  
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L1 0 FRT/FLP

=> s FRT or FLP  
L2 6180 FRT OR FLP

=> s cre lox  
L3 1238 CRE LOX

=> s l2 and stable recombination  
L4 0 L2 AND STABLE RECOMBINATION

=> s FRT ( ) FLP  
L5 96 FRT (W) FLP

=> s l5 and recombination  
L6 82 L5 AND RECOMBINATION

=> s 16 and stability  
L7 27 L6 AND STABILITY

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L7 ANSWER 1 OF 27 MEDLINE on STN

TI High-level heterologous gene expression in *Saccharomyces cerevisiae* from a stable 2 microns plasmid system.

AB The best candidate for a high-copy-number and mitotic **stability** expression system in yeast is the endogenous 2 microns plasmid. Nevertheless, derivatives of the 2 microns plasmid typically exhibit lower copy numbers and require selection for adequate maintenance within cells. We report the construction and utilization of an efficient heterologous gene expression system containing a 4.5-kb inducible expression cassette inserted into the 2 microns plasmid and selected in cells utilizing a carrier plasmid which is subsequently lost via **FRT/Flp recombination**. The non-selectable 2 micron plasmid, containing the cassette, was found to be stably maintained in cells, without selection, at high copy number. The dynamics of resolution and partitioning of this plasmid were analyzed during the course of 50 generations of growth under non-selective conditions. The heterologous lacZ reporter gene coding for beta-galactosidase (beta Gal) is driven by the hybrid, galactose-inducible promoter GAL10::pMF alpha 1. Upon induction, beta Gal was secreted into the periplasm and culture supernatant at levels which could be detected directly from Coomassie blue-stained SDS-PAGE. Furthermore, plasmid-containing cells could be maintained directly on rich YPD medium and identified either by utilizing XGal or by observing inhibition of colony growth on YPGal solid medium. The cassette was designed for direct, high-level, inducible expression of cloned genes downstream from the MF alpha 1 signal sequence, with or without a C-terminal lacZ fusion. This vector represents the first demonstration of a non-selectable, mitotically stable, episomal plasmid system capable of expressing recombinant proteins at high levels. (ABSTRACT TRUNCATED AT 250 WORDS)

ACCESSION NUMBER: 94010342 MEDLINE  
DOCUMENT NUMBER: PubMed ID: 8406040  
TITLE: High-level heterologous gene expression in *Saccharomyces cerevisiae* from a stable 2 microns plasmid system.  
AUTHOR: Ludwig D L; Ugolini S; Bruschi C V  
CORPORATE SOURCE: Microbiology Department, International Centre for Genetic Engineering and Biotechnology, Trieste, Italy.  
SOURCE: Gene, (1993 Sep 30) 132 (1) 33-40.  
Journal code: 7706761. ISSN: 0378-1119.  
PUB. COUNTRY: Netherlands  
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)  
LANGUAGE: English  
FILE SEGMENT: Priority Journals; Space Life Sciences  
ENTRY MONTH: 199311  
ENTRY DATE: Entered STN: 19940117  
Last Updated on STN: 19940117  
Entered Medline: 19931119

L7 ANSWER 2 OF 27 USPATFULL on STN

TI Modified starch metabolism enzymes and encoding genes for improvement and optimization of plant phenotypes

AB The invention provides methods for generating, identifying, and selecting polynucleotides encoding novel starch metabolizing enzymes (NSME), NSME-encoding polynucleotides, compositions of recombinant shuffled NSME protein, plant cells and microbes containing a shuffled NSME polynucleotide in expressible form, plants containing a shuffled NSME polynucleotide in expressible form, novel starch compositions produced by plants and cells, uses of such plants, cells, and starch compositions.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:59856 USPATFULL  
TITLE: Modified starch metabolism enzymes and encoding genes  
for improvement and optimization of plant phenotypes  
INVENTOR(S): Stemmer, Willem P. C., Los Gatos, CA, United States  
Subramanian, Venkiteswaran, San Diego, CA, United States  
Raillard, Sun Ai, Mountain View, CA, United States  
Huisman, Gjalte, San Carlos, CA, United States  
PATENT ASSIGNEE(S): Maxygar, Inc., Redwood City, CA, United States (U.S.  
corporation)

|                     | NUMBER         | KIND | DATE         |
|---------------------|----------------|------|--------------|
| PATENT INFORMATION: | US 6703240     | B1   | 20040309     |
| APPLICATION INFO.:  | US 2000-547844 |      | 20000412 (9) |

|                       | NUMBER   | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 1999-129009P  | 19990413 (60) |
| DOCUMENT TYPE:        | Utility  |               |
| FILE SEGMENT:         | GRANTED  |               |
| PRIMARY EXAMINER:     | Reynolds, Deborah J.   |               |
| ASSISTANT EXAMINER:   | Woitach, Joseph  |               |
| LEGAL REPRESENTATIVE: | Holmer, Christopher, Kruse, Norman J., Townsend &<br>Townsend & Crew |               |
| NUMBER OF CLAIMS:     | 82   |               |
| EXEMPLARY CLAIM:      | 1  |               |
| NUMBER OF DRAWINGS:   | 3 Drawing Figure(s); 3 Drawing Page(s)                               |               |
| LINE COUNT:           | 2972   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 3 OF 27 USPATFULL on STN

TI In vitro mutagenesis, phenotyping, and gene mapping  
AB Cellular libraries useful for in vitro phenotyping and gene mapping. In  
a representative approach, a method for preparing a homozygous cellular  
library includes the steps of providing a heterozygous cellular library  
comprising a plurality of isolated parent cells; inducing site-specific  
mitotic **recombination** in the plurality of isolated parent  
cells; culturing the plurality of isolated parent cells, whereby a  
population of daughter cells is produced; and selecting daughter cells  
comprising a homozygous genetic modification, whereby a homozygous  
cellular library is prepared.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:44603 USPATFULL  
TITLE: In vitro mutagenesis, phenotyping, and gene mapping  
INVENTOR(S): Threadgill, David W., Chapel Hill, NC, UNITED STATES  
Lee, Daekee, Chapel Hill, NC, UNITED STATES

|                     | NUMBER         | KIND | DATE          |
|---------------------|----------------|------|---------------|
| PATENT INFORMATION: | US 2004033596  | A1   | 20040219      |
| APPLICATION INFO.:  | US 2003-428977 | A1   | 20030502 (10) |

|                       | NUMBER  | DATE          |
|-----------------------|---|---------------|
| PRIORITY INFORMATION: | US 2002-377864P   | 20020502 (60) |
| DOCUMENT TYPE:        | Utility   |               |
| FILE SEGMENT:         | APPLICATION   |               |
| LEGAL REPRESENTATIVE: | JENKINS & WILSON, PA, 3100 TOWER BLVD, SUITE 1400,<br>DURHAM, NC, 27707 |               |
| NUMBER OF CLAIMS:     | 71  |               |
| EXEMPLARY CLAIM:      | 1   |               |



NUMBER OF DRAWINGS: 6 Drawing Page(s)  
LINE COUNT: 3125  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 4 OF 27 USPATFULL on STN

TI Self-rearranging DNA vectors

AB Disclosed are replicatable viral DNA vectors encoding a site-specific DNA-altering enzyme and a DNA target recognized by the enzyme, the enzyme selectively converting, in a cell expressing the enzyme, the DNA vector to a rearranged form. The invention further relates to methods for assembling recombinant adenoviral DNAs. These methods include the steps of: (a) providing a first linearized DNA vector including a restriction site and a cos site and a second linearized DNA vector including the restriction site, an adenoviral nucleic acid molecule, and a cos site; and (b) ligating the first and second linearized DNA vectors, the ligation assembling a recombinant adenoviral DNA.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:38117 USPATFULL

TITLE: Self-rearranging DNA vectors

INVENTOR(S): Seed, Brian, Boston, MA, UNITED STATES  
Freeman, Mason Wright, Lincoln, MA, UNITED STATES  
Kovtun, Alexander, Acton, MA, UNITED STATES  
Murakawa, Masahiro, Fukuoka City, JAPAN  
Park, Eun-Chung, Washington, DC, UNITED STATES  
Wang, Xinzong, Framingham, MA, UNITED STATES

|                       | NUMBER   | KIND | DATE          |
|-----------------------|--|------|---------------|
| PATENT INFORMATION:   | US 2004028653  | A1   | 20040212      |
| APPLICATION INFO.:    | US 2003-384136   | A1   | 20030307 (10) |
| RELATED APPLN. INFO.: | Continuation of Ser. No. WO 2001-US27682, filed on 7 Sep 2001, PENDING |      |               |

|                       | NUMBER  | DATE          |
|-----------------------|---|---------------|
| PRIORITY INFORMATION: | US 2000-246904P   | 20001108 (60) |
|                       | US 2000-231053P   | 20000908 (60) |
| DOCUMENT TYPE:        | Utility   |               |
| FILE SEGMENT:         | APPLICATION   |               |
| LEGAL REPRESENTATIVE: | CLARK & ELBING LLP, 101 FEDERAL STREET, BOSTON, MA, 02110 |               |
| NUMBER OF CLAIMS:     | 34  |               |
| EXEMPLARY CLAIM:      | 1   |               |
| NUMBER OF DRAWINGS:   | 40 Drawing Page(s)  |               |
| LINE COUNT:           | 3577  |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 5 OF 27 USPATFULL on STN

TI Compositions and methods for making mutations in cell lines and animals

AB The present invention is directed generally to reduction or inactivation of gene function or gene expression in cells in vitro and in multicellular organisms. The invention encompasses methods for mutating cells using a combination of mutagens, particularly wherein at least one mutagen is an insertional mutagen, to achieve homozygous gene mutation or mutation of multiple genes required cumulatively to achieve a phenotype to create knock-outs, knock-downs, and other modifications in the same cell. The invention is also directed to cells (and libraries thereof) and organisms created by the methods of the invention, including those in which at least one of the genes created by insertional mutagenesis is tagged by means of the insertion sequences thereby allowing identification of the mutated gene(s). The invention is also directed to libraries of mutated cells and their uses. The invention is also directed to methods of identifying mutations with

methods of the invention, in cells (and libraries thereof) and organisms, by means of the insertional tag.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:24785 USPATFULL  
TITLE: Compositions and methods for making mutations in cell lines and animals  
INVENTOR(S): Harrington, John Joseph, Mentor, OH, UNITED STATES  
Jackson, Paul David, Shaker Heights, OH, UNITED STATES  
Jiang, Li, Hudson, OH, UNITED STATES  
PATENT ASSIGNEE(S): Athersys, Inc., Cleveland, OH, 44115 (U.S. corporation)

|                       | NUMBER   | KIND | DATE          |
|-----------------------|--|------|---------------|
| PATENT INFORMATION:   | US 2004018624  | A1   | 20040129      |
| APPLICATION INFO.:    | US 2002-277612   | A1   | 20021022 (10) |
| RELATED APPLN. INFO.: | Continuation-in-part of Ser. No. US 2002-196721, filed on 15 Jul 2002, ABANDONED |      |               |

|                       | NUMBER   | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 2001-336497P  | 20011022 (60) |
| DOCUMENT TYPE:        | Utility  |               |
| FILE SEGMENT:         | APPLICATION  |               |
| LEGAL REPRESENTATIVE: | LAHIVE & COCKFIELD, 28 STATE STREET, BOSTON, MA, 02109 |               |
| NUMBER OF CLAIMS:     | 170  |               |
| EXEMPLARY CLAIM:      | 1  |               |
| NUMBER OF DRAWINGS:   | 21 Drawing Page(s)                                     |               |
| LINE COUNT:           | 4151   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 6 OF 27 USPATFULL on STN

TI Compositions and methods for the targeted insertion of a nucleotide sequence of interest into the genome of a plant

AB Methods for the targeted integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:3409 USPATFULL  
TITLE: Compositions and methods for the targeted insertion of a nucleotide sequence of interest into the genome of a plant  
INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, UNITED STATES  
Bowen, Benjamin A., Berkeley, CA, UNITED STATES  
Peterson, David J., Ames, IA, UNITED STATES  
Tagliani, Laura, Zionsville, IN, UNITED STATES  
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc. (U.S. corporation)

|                       | NUMBER   | KIND | DATE          |
|-----------------------|--|------|---------------|
| PATENT INFORMATION:   | US 2004003435  | A1   | 20040101      |
| APPLICATION INFO.:    | US 2003-440030   | A1   | 20030516 (10) |
| RELATED APPLN. INFO.: | Continuation of Ser. No. US 1999-455050, filed on 6 Dec 1999, GRANTED, Pat. No. US 6624297 Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, GRANTED, Pat. No. US 6187994 |      |               |

|  | NUMBER   | DATE          |
|--|--|---------------|
|  | -----  | -----         |
| PRIORITY INFORMATION:                      | US 1997-65627P   | 19971118 (60) |
|  | US 1997-65613P   | 19971118 (60) |
| DOCUMENT TYPE:                             | Utility  |               |
| FILE SEGMENT:                              | APPLICATION  |               |
| LEGAL REPRESENTATIVE:                      | ALSTON & BIRD LLP, PIONEER HI-BRED INTERNATIONAL, INC.,<br>BANK OF AMERICA PLAZA, 101 SOUTH TYRON STREET, SUITE<br>4000, CHARLOTTE, NC, 28280-4000 |               |
| NUMBER OF CLAIMS:                          | 22   |               |
| EXEMPLARY CLAIM:                           | 1  |               |
| NUMBER OF DRAWINGS:                        | 2 Drawing Page(s)  |               |
| LINE COUNT:                                | 1546   |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |

L7 ANSWER 7 OF 27 USPATFULL on STN

TI Compositions and methods to reduce the complexity of transgene integration into the genome of a plant

AB Methods for the targeted integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:336227 USPATFULL

TITLE: Compositions and methods to reduce the complexity of transgene integration into the genome of a plant

INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, UNITED STATES  
Bowen, Benjamin A., Berkeley, CA, UNITED STATES  
Peterson, David J., Ames, IA, UNITED STATES  
Tagliani, Laura, Zionsville, IN, UNITED STATES

PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc. (U.S. corporation)

|                       | NUMBER   | KIND  | DATE          |
|-----------------------|--|-------|---------------|
|                       | -----  | ----- | -----         |
| PATENT INFORMATION:   | US 2003237107  | A1    | 20031225      |
| APPLICATION INFO.:    | US 2003-430908   | A1    | 20030507 (10) |
| RELATED APPLN. INFO.: | Continuation of Ser. No. US 1999-455050, filed on 6 Dec 1999, GRANTED, Pat. No. US 6624297 Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, GRANTED, Pat. No. US 6187994 |       |               |

|  | NUMBER   | DATE          |
|--|--|---------------|
|  | -----  | -----         |
| PRIORITY INFORMATION:                      | US 1997-65627P   | 19971118 (60) |
|  | US 1997-65613P   | 19971118 (60) |
| DOCUMENT TYPE:                             | Utility  |               |
| FILE SEGMENT:                              | APPLICATION  |               |
| LEGAL REPRESENTATIVE:                      | ALSTON & BIRD LLP, PIONEER HI-BRED INTERNATIONAL, INC.,<br>BANK OF AMERICA PLAZA, 101 SOUTH TYRON STREET, SUITE<br>4000, CHARLOTTE, NC, 28280-4000 |               |
| NUMBER OF CLAIMS:                          | 23   |               |
| EXEMPLARY CLAIM:                           | 1  |               |
| NUMBER OF DRAWINGS:                        | 2 Drawing Page(s)  |               |
| LINE COUNT:                                | 1556   |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |

L7 ANSWER 8 OF 27 USPATFULL on STN

TI Compositions and methods for locating preferred integration sites within

the genome of a plant

AB Methods to find optimal integration sites within a plant genome are provided. More particularly, a plant is transformed with a target site having an expression cassette comprising a nucleotide sequence operably linked to a promoter active in the plant. The target site is flanked by non-identical **recombination** sites. Transformed protoplast, tissues, or whole plants can be tested to determine the levels of activity of the inserted gene. By comparison of cellular activities of the gene in different insertion sites, preferred integration sites may be found wherein the gene is expressed at high or acceptable levels. These plants can then be utilized with subsequent retargeting techniques to replace the nucleotide sequence with other genes or nucleotide sequences of interest contained in a transfer cassette.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:320407 USPATFULL

TITLE: Compositions and methods for locating preferred integration sites within the genome of a plant

INVENTOR(S): Baszczyński, Christopher L., Urbandale, IA, UNITED STATES

Bowen, Benjamin A., Berkeley, CA, UNITED STATES

Peterson, David J., Ames, IA, UNITED STATES

Tagliani, Laura, Zionsville, IN, UNITED STATES

PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc. (U.S. corporation)

|                       | NUMBER   | KIND | DATE          |
|-----------------------|--|------|---------------|
| PATENT INFORMATION:   | US 2003226160  | A1   | 20031204      |
| APPLICATION INFO.:    | US 2003-430907   | A1   | 20030507 (10) |
| RELATED APPLN. INFO.: | Continuation of Ser. No. US 1999-455050, filed on 6 Dec 1999, GRANTED, Pat. No. US 6624297 Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, GRANTED, Pat. No. US 6187994 |      |               |

|                       | NUMBER   | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 1997-65627P   | 19971118 (60) |
|                       | US 1997-65613P   | 19971118 (60) |
| DOCUMENT TYPE:        | Utility  |               |
| FILE SEGMENT:         | APPLICATION  |               |
| LEGAL REPRESENTATIVE: | ALSTON & BIRD LLP, PIONEER HI-BRED INTERNATIONAL, INC., BANK OF AMERICA PLAZA, 101 SOUTH TYRON STREET, SUITE 4000, CHARLOTTE, NC, 28280-4000 |               |
| NUMBER OF CLAIMS:     | 17   |               |
| EXEMPLARY CLAIM:      | 1  |               |
| NUMBER OF DRAWINGS:   | 2 Drawing Page(s)  |               |
| LINE COUNT:           | 1537   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 9 OF 27 USPATFULL on STN

TI Compositions and methods for making mutations in cell lines and animals

AB The present invention is directed generally to reduction or inactivation of gene function or gene expression in cells in vitro and in multicellular organisms. The invention encompasses methods for mutating cells using a combination of mutagens, particularly wherein at least one mutagen is an insertional mutagen, to achieve homozygous gene mutation or mutation of multiple genes required cumulatively to achieve a phenotype to create knock-outs, knock-downs, and other modifications in the same cell. The invention is also directed to cells (and libraries thereof) and organisms created by the methods of the invention, including those in which at least one of the genes created by insertional mutagenesis is tagged by means of the insertion sequences thereby allowing identification of the mutated gene(s). The invention is also directed to libraries of mutated cells and their uses. The

invention is also directed to methods of identifying mutations with methods of the invention, in cells (and libraries thereof) and organisms, by means of the insertional tag.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:318774 USPATFULL  
TITLE: Compositions and methods for making mutations in cell lines and animals  
INVENTOR(S): Harrington, John Joseph, Mentor, OH, UNITED STATES  
Jackson, Paul David, Shaker Heights, OH, UNITED STATES  
Jiang, Li, Hudson, OH, UNITED STATES  
PATENT ASSIGNEE(S): Athersys, Inc., Cleveland, OH (U.S. corporation)

|                       | NUMBER  | KIND | DATE          |
|-----------------------|---|------|---------------|
| PATENT INFORMATION:   | US 2003224519   | A1   | 20031204      |
| APPLICATION INFO.:    | US 2003-345115  | A1   | 20030115 (10) |
| RELATED APPLN. INFO.: | Continuation-in-part of Ser. No. US 2002-277612, filed on 22 Oct 2002, PENDING Continuation-in-part of Ser. No. US 2002-196721, filed on 15 Jul 2002, ABANDONED |      |               |

|                       | NUMBER   | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 2001-336497P  | 20011022 (60) |
| DOCUMENT TYPE:        | Utility  |               |
| FILE SEGMENT:         | APPLICATION  |               |
| LEGAL REPRESENTATIVE: | LAHIVE & COCKFIELD, 28 STATE STREET, BOSTON, MA, 02109 |               |
| NUMBER OF CLAIMS:     | 210  |               |
| EXEMPLARY CLAIM:      | 1  |               |
| NUMBER OF DRAWINGS:   | 21 Drawing Page(s)                                     |               |
| LINE COUNT:           | 4363   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 10 OF 27 USPATFULL on STN

TI DNA sequences comprising gene transcription regulatory qualities and methods for detecting and using such DNA sequences

AB The invention is concerned with the systematic elucidation and identification of regulatory sequences. The invention provides among others screenings and detection methods with which regulatory sequences can be identified. The invention further provides regulatory sequences and use thereof in various fields such as, but not limited to protein production, diagnostics, transgenic plants and animals, and the therapeutic field.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:283124 USPATFULL  
TITLE: DNA sequences comprising gene transcription regulatory qualities and methods for detecting and using such DNA sequences  
INVENTOR(S): Otte, Arie Peter, Purmerend, NETHERLANDS  
Kruckeberg, Arthur Leo, Amsterdam, NETHERLANDS

|                     | NUMBER         | KIND | DATE          |
|---------------------|----------------|------|---------------|
| PATENT INFORMATION: | US 2003199468  | A1   | 20031023      |
| APPLICATION INFO.:  | US 2002-190312 | A1   | 20020705 (10) |

|                       | NUMBER  | DATE          |
|-----------------------|---|---------------|
| PRIORITY INFORMATION: | US 2001-303199P                                       | 20010705 (60) |
| DOCUMENT TYPE:        | Utility   |               |
| FILE SEGMENT:         | APPLICATION   |               |
| LEGAL REPRESENTATIVE: | TRASK BRITT, P.O. BOX 2550, SALT LAKE CITY, UT, 84110 |               |
| NUMBER OF CLAIMS:     | 77  |               |

EXEMPLARY CLAIM: 1  
NUMBER OF DRAWINGS: 65 Drawing Page(s)  
LINE COUNT: 4902  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 11 OF 27 USPATFULL on STN  
TI Compositions for the genetic modification of plants  
AB Methods and compositions for the targeted integration of nucleotide sequences into a plant are provided. Particularly, the present invention is drawn to compositions comprising polynucleotide sequences having the following operably linked components: an intron, a nucleotide sequence of interest, and a terminator region, wherein the polynucleotide sequence comprises one or more **recombination** sites. The **recombination** sites are non-identical to one another and one of the **recombination** sites is contained within the intron.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:253688 USPATFULL  
TITLE: Compositions for the genetic modification of plants  
INVENTOR(S): Baszczyński, Christopher L., Urbandale, IA, United States  
Bowen, Benjamin A., Des Moines, IA, United States  
Peterson, David J., Ames, IA, United States  
Tagliani, Laura A., Ankeny, IA, United States  
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

|                       | NUMBER  | KIND | DATE         |
|-----------------------|---|------|--------------|
| PATENT INFORMATION:   | US 6624297  | B1   | 20030923     |
| APPLICATION INFO.:    | US 1999-455050  |      | 19991206 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, now patented, Pat. No. US 6187994, issued on 13 Feb 2001 |      |              |

|                       | NUMBER                                 | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 1997-65627P                         | 19971118 (60) |
|                       | US 1997-65613P                         | 19971118 (60) |
| DOCUMENT TYPE:        | Utility                                |               |
| FILE SEGMENT:         | GRANTED                                |               |
| PRIMARY EXAMINER:     | Fox, David T.                          |               |
| ASSISTANT EXAMINER:   | Kruse, David H                         |               |
| LEGAL REPRESENTATIVE: | Alston & Bird LLP                      |               |
| NUMBER OF CLAIMS:     | 15                                     |               |
| EXEMPLARY CLAIM:      | 1                                      |               |
| NUMBER OF DRAWINGS:   | 2 Drawing Figure(s); 2 Drawing Page(s) |               |
| LINE COUNT:           | 1599                                   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 12 OF 27 USPATFULL on STN  
TI Compositions and methods to reduce the complexity of transgene integration in the genome of a plant  
AB Methods for reducing the complexity of integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:149071 USPATFULL

TITLE: Compositions and methods to reduce the complexity of  
transgene integration in the genome of a plant  
INVENTOR(S): Baszczyński, Christopher L., Urbandale, IA, United  
States  
Bowen, Benjamin A., Des Moines, IA, United States  
Peterson, David J., Ames, IA, United States  
Tagliani, Laura A., Ankeny, IA, United States  
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA,  
United States (U.S. corporation)

|                       | NUMBER  | KIND | DATE         |
|-----------------------|---|------|--------------|
| PATENT INFORMATION:   | US 6573425  | B1   | 20030603     |
| APPLICATION INFO.:    | US 1999-439042  |      | 19991112 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1998-193502, filed on 17 Nov<br>1998, now patented, Pat. No. US 6187994 |      |              |

|  | NUMBER                                 | DATE          |
|--|--|---------------|
| PRIORITY INFORMATION:                      | US 1997-65627P                         | 19971118 (60) |
|  | US 1997-65613P                         | 19971118 (60) |
| DOCUMENT TYPE:                             | Utility                                |               |
| FILE SEGMENT:                              | GRANTED                                |               |
| PRIMARY EXAMINER:                          | Fox, David T.                          |               |
| ASSISTANT EXAMINER:                        | Kruse, David H                         |               |
| LEGAL REPRESENTATIVE:                      | Alston & Bird LLP                      |               |
| NUMBER OF CLAIMS:                          | 37                                     |               |
| EXEMPLARY CLAIM:                           | 1                                      |               |
| NUMBER OF DRAWINGS:                        | 2 Drawing Figure(s); 2 Drawing Page(s) |               |
| LINE COUNT:                                | 1650                                   |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |

L7 ANSWER 13 OF 27 USPATFULL on STN

TI Universal stem cells

AB The subject invention pertains to materials and methods for preparing multi-potential stem cells having a pre-selected expression of MHC antigens. Stem cells of the subject invention can be used to generate histocompatible tissues/organs for transplantation. The process of the subject invention comprises the use of targeting vectors capable of gene knockout, insertion of site-specific **recombination** cassettes, and the replacement of histocompatibility alleles in the stem cell. Novel knockout vectors are used to delete designated regions of one chromosome. **Recombination** cassette vectors are then used to delete the same region on the second chromosome and deposit a site-specific **recombination** cassette which can be utilized by replacement vectors for inserting the new MHC genes on the chromosome of the engineered cell. The subject invention also pertains to cells, tissues, and transgenic mammal prepared using the methods and materials of the invention.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:147717 USPATFULL

TITLE: Universal stem cells

INVENTOR(S): Lawman, Patricia, Chipley, FL, UNITED STATES  
Lawman, Michael J.P., Chipley, FL, UNITED STATES

|                       | NUMBER   | KIND | DATE          |
|-----------------------|--|------|---------------|
| PATENT INFORMATION:   | US 2003101465  | A1   | 20030529      |
| APPLICATION INFO.:    | US 2002-186231   | A1   | 20020628 (10) |
| RELATED APPLN. INFO.: | Continuation of Ser. No. US 1998-47769, filed on 25 Mar<br>1998, ABANDONED |      |               |

| NUMBER | DATE |
|--------|------|
|--------|------|

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PRIORITY INFORMATION: US 1997-42358P 19970325 (60)  
DOCUMENT TYPE: Utility  
FILE SEGMENT: APPLICATION  
LEGAL REPRESENTATIVE: SALIWANCHIK LLOYD & SALIWANCHIK, A PROFESSIONAL  
ASSOCIATION, 2421 N.W. 41ST STREET, SUITE A-1,  
GAINESVILLE, FL, 326066669

NUMBER OF CLAIMS: 18  
EXEMPLARY CLAIM: 1  
NUMBER OF DRAWINGS: 6 Drawing Page(s)  
LINE COUNT: 1852  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 14 OF 27 USPATFULL on STN  
TI Compositions and methods for locating preferred integration sites within  
a plant genome  
AB Methods to find optimal integration sites within a plant genome are  
provided. More particularly, a plant is transformed with a target site  
having an expression cassette comprising a nucleotide sequence operably  
linked to a promoter active in the plant. The target site is flanked by  
non-identical **recombination** sites, Transformed protoplast,  
tissues, or whole plants can be tested to determine the levels of  
activity of the inserted gene, By comparison of cellular activities of  
the gene in different insertion sites, preferred integration sites may  
be found wherein the gene is expressed at high or acceptable levels.  
These plants can then be utilized with subsequent retargeting techniques  
to replace the nucleotide sequence with other genes or nucleotide  
sequences of interest contained in a transfer cassette.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
ACCESSION NUMBER: 2003:109223 USPATFULL  
TITLE: Compositions and methods for locating preferred  
integration sites within a plant genome  
INVENTOR(S): Baszczyński, Christopher L., Urbandale, IA, United  
States  
Bowen, Benjamin A., Des Moines, IA, United States  
Peterson, David J., Ames, IA, United States  
Tagliani, Laura A., Ankeny, IA, United States  
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA,  
United States (U.S. corporation)

|                       | NUMBER  | KIND | DATE         |
|-----------------------|---|------|--------------|
| PATENT INFORMATION:   | US 6552248  | B1   | 20030422     |
| APPLICATION INFO.:    | US 1999-438239  |      | 19991112 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1998-193502, filed on 17 Nov<br>1998, now patented, Pat. No. US 6187994, issued on 13<br>Feb 2001 |      |              |

|  | NUMBER                                 | DATE          |
|--|--|---------------|
| PRIORITY INFORMATION:                      | US 1997-65627P                         | 19971118 (60) |
|  | US 1997-65613P                         | 19971118 (60) |
| DOCUMENT TYPE:                             | Utility                                |               |
| FILE SEGMENT:                              | GRANTED                                |               |
| PRIMARY EXAMINER:                          | Fox, David T.                          |               |
| ASSISTANT EXAMINER:                        | Kruse, David H                         |               |
| LEGAL REPRESENTATIVE:                      | Alston & Bird LLP                      |               |
| NUMBER OF CLAIMS:                          | 49                                     |               |
| EXEMPLARY CLAIM:                           | 1                                      |               |
| NUMBER OF DRAWINGS:                        | 2 Drawing Figure(s); 2 Drawing Page(s) |               |
| LINE COUNT:                                | 1684                                   |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |



L7 ANSWER 15 OF 27 USPATFULL on STN  
TI Methods for improving a photosynthetic carbon fixation enzyme  
AB The invention relates to methods and compositions for generating, modifying, adapting, and optimizing polynucleotide sequences that encode proteins having photosynthetic carbon fixation activities, including Rubisco and Rubisco activase activities, which are useful for introduction into plant species, agronomically-important microorganisms, and other hosts, and related aspects.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:106224 USPATFULL  
TITLE: Methods for improving a photosynthetic carbon fixation enzyme  
INVENTOR(S): Zhu, Genhai, San Jose, CA, UNITED STATES  
PATENT ASSIGNEE(S): Maxygen, Inc. (U.S. corporation)

|                     | NUMBER         | KIND | DATE          |
|---------------------|----------------|------|---------------|
| PATENT INFORMATION: | US 2003073135  | A1   | 20030417      |
| APPLICATION INFO.:  | US 2002-271019 | A1   | 20021015 (10) |

|                       | NUMBER   | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 2001-328871P  | 20011012 (60) |
| DOCUMENT TYPE:        | Utility  |               |
| FILE SEGMENT:         | APPLICATION  |               |
| LEGAL REPRESENTATIVE: | MAXYGEN, INC., INTELLECTUAL PROPERTY DEPARTMENT, 515 GALVESTON DRIVE, RED WOOD CITY, CA, 94063 |               |
| NUMBER OF CLAIMS:     | 20   |               |
| EXEMPLARY CLAIM:      | 1  |               |
| LINE COUNT:           | 2569   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 16 OF 27 USPATFULL on STN  
TI Modified ADP-glucose pyrophosphorylase for improvement and optimization of plant phenotypes  
AB The invention provides methods and compositions relating to sequence-shuffled variants of ADP-glucose pyrophosphorylase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:304117 USPATFULL  
TITLE: Modified ADP-glucose pyrophosphorylase for improvement and optimization of plant phenotypes  
INVENTOR(S): Stemmer, Willem P. C., Los Gatos, CA, United States  
Subramanian, Venkiteswaran, San Diego, CA, United States  
PATENT ASSIGNEE(S): Maxygen, Inc., Redwood City, CA, United States (U.S. corporation)

|                       | NUMBER  | KIND | DATE         |
|-----------------------|---|------|--------------|
| PATENT INFORMATION:   | US 6483011  | B1   | 20021119     |
| APPLICATION INFO.:    | US 2000-721540  |      | 20001122 (9) |
| RELATED APPLN. INFO.: | Continuation of Ser. No. US 1999-437725, filed on 9 Nov 1999, now abandoned |      |              |

|                       | NUMBER                             | DATE          |
|-----------------------|------------------------------------|---------------|
| PRIORITY INFORMATION: | US 1998-107782P                    | 19981110 (60) |
| DOCUMENT TYPE:        | Utility                            |               |
| FILE SEGMENT:         | GRANTED                            |               |
| PRIMARY EXAMINER:     | Horlick, Kenneth R.                |               |
| ASSISTANT EXAMINER:   | Strzelecka, Teresa                 |               |
| LEGAL REPRESENTATIVE: | Townsend and Townsend and Crew LLP |               |

NUMBER OF CLAIMS: 17  
EXEMPLARY CLAIM: 1  
NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)  
LINE COUNT: 2975  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 17 OF 27 USPATFULL on STN  
TI Alpha-tocopherol transfer protein knockout animals  
AB This invention provides knockout animals comprising a disruption in one or both alleles of the gene encoding alpha-tocopherol transfer protein (TTP). The knockout animals provide good model systems for atherosclerosis.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:302526 USPATFULL  
TITLE: Alpha-tocopherol transfer protein knockout animals  
INVENTOR(S): Farese, Robert V., JR., San Francisco, CA, UNITED STATES  
Terasawa, Yuko, Campbell, CA, UNITED STATES  
Traber, Maret G., Corvallis, OR, UNITED STATES  
PATENT ASSIGNEE(S): The Regents of the University of California (U.S. corporation)

|                     | NUMBER        | KIND | DATE          |
|---------------------|---------------|------|---------------|
| PATENT INFORMATION: | US 2002170080 | A1   | 20021114      |
| APPLICATION INFO.:  | US 2001-1278  | A1   | 20011101 (10) |

|                       | NUMBER   | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 2000-245302P  | 20001102 (60) |
| DOCUMENT TYPE:        | Utility  |               |
| FILE SEGMENT:         | APPLICATION  |               |
| LEGAL REPRESENTATIVE: | QUINE INTELLECTUAL PROPERTY LAW GROUP, P.C., P O BOX 458, ALAMEDA, CA, 94501 |               |
| NUMBER OF CLAIMS:     | 56   |               |
| EXEMPLARY CLAIM:      | 1  |               |
| NUMBER OF DRAWINGS:   | 4 Drawing Page(s)  |               |
| LINE COUNT:           | 1912   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 18 OF 27 USPATFULL on STN  
TI METHODS FOR OBTAINING A POLYNECLEOTIDE ENCODING A POLYPEPTIDE HAVING A RUBISCO ACTIVITY  
AB The invention relates to methods and compositions for generating, modifying, adapting, and optimizing polynucleotide sequences that encode proteins having Rubisco biosynthetic enzyme activities which are useful for introduction into plant species, agronomically-important microorganisms, and other hosts, and related aspects.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:272896 USPATFULL  
TITLE: METHODS FOR OBTAINING A POLYNECLEOTIDE ENCODING A POLYPEPTIDE HAVING A RUBISCO ACTIVITY  
INVENTOR(S): STEMMER, WILLEM P. C., LOS GATOS, CA, UNITED STATES  
SUBRAMANIAN, VENKITSWARAN, SAN DIEGO, CA, UNITED STATES  
ZHU, GENHAI, SUNNYVALE, CA, UNITED STATES  
LIU, LU, REDWOOD CITY, CA, UNITED STATES  
SELIFONOV, SERGEY A., LOS ALTOS, CA, UNITED STATES

|                     | NUMBER         | KIND | DATE         |
|---------------------|----------------|------|--------------|
| PATENT INFORMATION: | US 2002151017  | A1   | 20021017     |
| APPLICATION INFO.:  | US 1999-437726 | A1   | 19991109 (9) |

|  | NUMBER   | DATE          |
|--|--|---------------|
|  | -----  | -----         |
| PRIORITY INFORMATION:                      | US 1999-153093P  | 19990909 (60) |
|  | US 1998-107756P  | 19981110 (60) |
| DOCUMENT TYPE:                             | Utility  |               |
| FILE SEGMENT:                              | APPLICATION  |               |
| LEGAL REPRESENTATIVE:                      | TOWNSEND AND TOWNSEND AND CREW, LLP, TWO EMBARCADERO CENTER, EIGHTH FLOOR, SAN FRANCISCO, CA, 94111-3834 |               |
| NUMBER OF CLAIMS:                          | 26   |               |
| EXEMPLARY CLAIM:                           | 1  |               |
| NUMBER OF DRAWINGS:                        | 5 Drawing Page(s)  |               |
| LINE COUNT:                                | 3434   |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |

L7 ANSWER 19 OF 27 USPATFULL on STN

TI Compositions and methods for the targeted removal of a nucleotide sequence from the genome of a plant

AB Methods and compositions to remove a nucleotide sequence of interest in a plant and plant cell are provided. In particular the methods of the invention comprise providing a plant cell having stably incorporated into its genome a transfer cassette comprising a nucleotide sequence of interest flanked by non-identical **recombination** sites and introducing into the plant cell a chimeric RNA-DNA oligonucleotide molecule. The chimeric RNA-DNA oligonucleotide is capable of recognizing and implementing a nucleotide conversion in one of the non-identical **recombination** sites so as to create two identical **recombination** sites. An appropriate recombinase is provided which excises the sequences between the two identical **recombination** sites.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:254223 USPATFULL

TITLE: Compositions and methods for the targeted removal of a nucleotide sequence from the genome of a plant

INVENTOR(S): Baszczyński, Christopher L., Urbandale, IA, United States  
Bowen, Benjamin A., Berkeley, CA, United States  
Peterson, David J., Ames, IA, United States  
Tagliani, Laura A., Zionsville, IN, United States

PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

|                       | NUMBER  | KIND  | DATE         |
|-----------------------|---|-------|--------------|
|                       | -----   | ----- | -----        |
| PATENT INFORMATION:   | US 6458594  | B1    | 20021001     |
| APPLICATION INFO.:    | US 1999-439158  |       | 19991112 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, now patented, Pat. No. US 6187994, issued on 13 Feb 2001 |       |              |

|                       | NUMBER            | DATE          |
|-----------------------|-------------------|---------------|
|                       | -----             | -----         |
| PRIORITY INFORMATION: | US 1997-65627P    | 19971118 (60) |
|                       | US 1997-65613P    | 19971118 (60) |
|                       | US 1998-98235P    | 19980828 (60) |
|                       | US 1997-65628P    | 19971118 (60) |
| DOCUMENT TYPE:        | Utility           |               |
| FILE SEGMENT:         | GRANTED           |               |
| PRIMARY EXAMINER:     | Fox, David T.     |               |
| ASSISTANT EXAMINER:   | Kruse, David H    |               |
| LEGAL REPRESENTATIVE: | Alston & Bird LLP |               |
| NUMBER OF CLAIMS:     | 30                |               |
| EXEMPLARY CLAIM:      | 1                 |               |

NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)  
LINE COUNT: 1619  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 20 OF 27 USPATFULL on STN

TI Compositions and methods to stack multiple nucleotide sequences of interest in the genome of a plant  
AB Methods and compositions for the stacking of multiple nucleotide sequences at precise locations in the genome of a plant or plant cell are provided, Specifically, transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase. The transfer cassettes and target sites are designed so as to allow for the stacking or ordering of nucleotide sequences at precise locations in the plant genome.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:246589 USPATFULL  
TITLE: Compositions and methods to stack multiple nucleotide sequences of interest in the genome of a plant  
INVENTOR(S): Baszczyński, Christopher L., Urbandale, IA, United States  
Bowen, Benjamin A., Des Moines, IA, United States  
Peterson, David J., Ames, IA, United States  
Tagliani, Laura A., Ankeny, IA, United States  
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

|                       | NUMBER  | KIND | DATE         |
|-----------------------|---|------|--------------|
| PATENT INFORMATION:   | US 6455315  | B1   | 20020924     |
| APPLICATION INFO.:    | US 1999-438874  |      | 19991112 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1998-193502, filed on 17 Nov 1998, now patented, Pat. No. US 6187994, issued on 13 Feb 2000 |      |              |

|                       | NUMBER         | DATE          |
|-----------------------|----------------|---------------|
| PRIORITY INFORMATION: | US 1997-65627P | 19971118 (60) |
|                       | US 1997-65613P | 19971118 (60) |

DOCUMENT TYPE: Utility  
FILE SEGMENT: GRANTED  
PRIMARY EXAMINER: Fox, David T.  
ASSISTANT EXAMINER: Kruse, David H  
LEGAL REPRESENTATIVE: Alston & Bird LLP  
NUMBER OF CLAIMS: 44  
EXEMPLARY CLAIM: 1  
NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)  
LINE COUNT: 1695  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 21 OF 27 USPATFULL on STN

TI Modified ribulose 1,5-bisphosphate carboxylase/oxygenase for improvement and optimization of plant phenotypes  
AB The invention relates to methods and compositions for generating, modifying, adapting, and optimizing polynucleotide sequences that encode proteins having Rubisco biosynthetic enzyme activities which are useful for, introduction into plant species, agronomically-important microorganisms, and other hosts, and related aspects.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2001:183179 USPATFULL  
TITLE: Modified ribulose 1,5-bisphosphate  
carboxylase/oxygenase for improvement and optimization  
of plant phenotypes  
INVENTOR(S): Stemmer, Willem P.C., Los Gatos, CA, United States  
Subramanian, Venkiteswaran, San Diego, CA, United States  
Zhu, Genhai, Sunnyvale, CA, United States  
Liu, Lu, Redwood City, CA, United States  
Selifonov, Sergey A., Los Altos, CA, United States  
PATENT ASSIGNEE(S): Maxygen. Inc. (U.S. corporation)

|                       | NUMBER  | KIND | DATE         |
|-----------------------|---|------|--------------|
| PATENT INFORMATION:   | US 2001032342   | A1   | 20011018     |
| APPLICATION INFO.:    | US 2001-800123  | A1   | 20010305 (9) |
| RELATED APPLN. INFO.: | Continuation of Ser. No. US 1999-437726, filed on 9 Nov 1999, PENDING |      |              |

|  | NUMBER   | DATE          |
|--|--|---------------|
| PRIORITY INFORMATION:                      | US 1999-153093P  | 19990909 (60) |
|  | US 1998-107756P  | 19981110 (60) |
| DOCUMENT TYPE:                             | Utility  |               |
| FILE SEGMENT:                              | APPLICATION  |               |
| LEGAL REPRESENTATIVE:                      | LAW OFFICES OF JONATHAN ALAN QUINE, P O BOX 458,<br>ALAMEDA, CA, 94501 |               |
| NUMBER OF CLAIMS:                          | 26   |               |
| EXEMPLARY CLAIM:                           | 1  |               |
| NUMBER OF DRAWINGS:                        | 5 Drawing Page(s)  |               |
| LINE COUNT:                                | 3440   |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |

L7 ANSWER 22 OF 27 USPATFULL on STN  
TI Compositions and methods for genetic modification of plants  
AB Methods for the targeted integration of nucleotide sequences into a plant are provided. Transfer cassettes comprising nucleotide sequences of interest flanked by non-identical **recombination** sites are used to transform a plant comprising a target site. The target site contains at least a set of non-identical **recombination** sites corresponding to those on the transfer cassette. Exchange of the nucleotide sequences flanked by the **recombination** sites is effected by a recombinase.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
ACCESSION NUMBER: 2001:22439 USPATFULL  
TITLE: Compositions and methods for genetic modification of plants  
INVENTOR(S): Baszczynski, Christopher L., Urbandale, IA, United States  
Bowen, Benjamin A., Des Moines, IA, United States  
Peterson, David J., Ames, IA, United States  
Tagliani, Laura A., Ankeny, IA, United States  
PATENT ASSIGNEE(S): Pioneer Hi-Bred International, Inc., Des Moines, IA, United States (U.S. corporation)

|                       | NUMBER   | KIND | DATE         |
|-----------------------|--|------|--------------|
| PATENT INFORMATION:   | US 6187994   | B1   | 20010213     |
| APPLICATION INFO.:    | US 1998-193502   |      | 19981117 (9) |
| RELATED APPLN. INFO.: | Continuation of Ser. No. US 1997-65627, filed on 18 Nov 1997<br>Continuation of Ser. No. US 1997-65613, filed on 18 Nov 1997 |      |              |

| NUMBER | DATE |
|--------|------|
|--------|------|

PRIORITY INFORMATION: US 1997-45121P 19970430 (60)  
 DOCUMENT TYPE: Utility  
 FILE SEGMENT: Granted  
 PRIMARY EXAMINER: McElwain, Elizabeth F.  
 ASSISTANT EXAMINER: Mehta, Ashwin D.  
 LEGAL REPRESENTATIVE: Alston & Bird LLP  
 NUMBER OF CLAIMS: 28  
 EXEMPLARY CLAIM: 1  
 NUMBER OF DRAWINGS: 2 Drawing Figure(s); 2 Drawing Page(s)  
 LINE COUNT: 1628  
 CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 23 OF 27 USPATFULL on STN

TI Mammalian artificial chromosomes and methods of using same  
 AB The present invention provides a mammalian artificial chromosome (MAC), comprising a centromere and a unique cloning site, said MAC containing less than 0.1% of the DNA present in a normal haploid genome of the mammalian cell from which the centromere was obtained. The invention further provides a MAC, wherein the unique cloning site is a nucleic acid sequence encoding a selectable marker. The invention also provides methods of preparing a MAC. In addition, the invention provides methods of stably expressing a selectable marker in a cell, comprising introducing a MAC containing the selectable marker into the cell. The invention also provides a cell containing a MAC expressing an exogenous nucleic acid sequence and a transgenic mammal expressing a selectable marker.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2000:138587 USPATFULL  
 TITLE: Mammalian artificial chromosomes and methods of using same  
 INVENTOR(S): Scheffler, Immo E., Del Mar, CA, United States  
 PATENT ASSIGNEE(S): The Regents of the University of California, Oakland, CA, United States (U.S. corporation)

|                       | NUMBER   | KIND | DATE         |
|-----------------------|--|------|--------------|
| PATENT INFORMATION:   | US 6133503   |      | 20001017     |
| APPLICATION INFO.:    | US 1998-24472  |      | 19980217 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1996-741406, filed on 29 Oct 1996, now patented, Pat. No. US 5721118 |      |              |

|                       | NUMBER                                 | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 1995-39256P                         | 19951031 (60) |
| DOCUMENT TYPE:        | Utility                                |               |
| FILE SEGMENT:         | Granted                                |               |
| PRIMARY EXAMINER:     | Campbell, Bruce R.                     |               |
| ASSISTANT EXAMINER:   | Woitach, Joseph                        |               |
| LEGAL REPRESENTATIVE: | Campbell & Flores LLP                  |               |
| NUMBER OF CLAIMS:     | 14                                     |               |
| EXEMPLARY CLAIM:      | 1                                      |               |
| NUMBER OF DRAWINGS:   | 6 Drawing Figure(s); 3 Drawing Page(s) |               |
| LINE COUNT:           | 1897                                   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 24 OF 27 USPATFULL on STN

TI Mice homozygous for an inactivated  $\alpha$  1,3-galactosyl transferase gene  
 AB Human pre-formed xenoantibodies play an important role in the hyperacute rejection response in human xenotransplantation. Disclosed are materials and methods for removing or neutralizing such antibodies. Also disclosed are materials and methods for reducing or eliminating the epitopes in

the donor organs that are recognized by such antibodies. Such epitopes are formed as the result of activity by the enzyme  $\alpha$ -1,3 galactosyltransferase. The porcine gene encoding  $\alpha$ -1,3 galactosyltransferase is disclosed, as are materials and methods for inactivating ("knocking out") the  $\alpha$ -1,3 galactosyltransferase gene in mammalian cells and embryos. Included are nucleic acid constructs useful for inactivating the  $\alpha$ -1,3 galactosyltransferase gene in a target cell. Also disclosed is a novel leukemia inhibitory factor (T-LIF) that is useful for maintenance of embryonic stem cells and primordial germ cells in culture.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 1998:157587 USPATFULL  
 TITLE: Mice homozygous for an inactivated  $\alpha$  1,3-galactosyl transferase gene  
 INVENTOR(S): d'Apice, Anthony J. F., Balwyn, Australia  
 Pearse, Martin J., Mordialloc, Australia  
 Robins, Allan J., Waterloo Corner, Australia  
 Crawford, Robert J., West Lake Shores, Australia  
 Rathjen, Peter D., Blackwood, Australia  
 PATENT ASSIGNEE(S): Bresatch Limited, Adelaide, Australia (non-U.S. corporation)  
 St. Vincent's Hospital, Victoria, Australia (non-U.S. corporation)

|                       | NUMBER   | KIND | DATE         |
|-----------------------|--|------|--------------|
| PATENT INFORMATION:   | US 5849991   |      | 19981215     |
| APPLICATION INFO.:    | US 1995-378617   |      | 19950126 (8) |
| RELATED APPLN. INFO.: | Continuation-in-part of Ser. No. US 1994-188607, filed on 27 Jan 1994, now abandoned |      |              |
| DOCUMENT TYPE:        | Utility  |      |              |
| FILE SEGMENT:         | Granted  |      |              |
| PRIMARY EXAMINER:     | Crouch, Deborah  |      |              |
| LEGAL REPRESENTATIVE: | Fish & Richardson P.C., P.A.   |      |              |
| NUMBER OF CLAIMS:     | 13   |      |              |
| EXEMPLARY CLAIM:      | 5  |      |              |
| NUMBER OF DRAWINGS:   | 47 Drawing Figure(s); 42 Drawing Page(s)   |      |              |
| LINE COUNT:           | 4190   |      |              |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 25 OF 27 USPATFULL on STN

TI Mammalian artificial chromosomes and methods of using same  
 AB The present invention provides a mammalian artificial chromosome (MAC), comprising a centromere and a unique cloning site, said MAC containing less than 0.1% of the DNA present in a normal haploid genome of the mammalian cell from which the centromere was obtained. The invention further provides a MAC, wherein the unique cloning site is a nucleic acid sequence encoding a selectable marker. The invention also provides methods of preparing a MAC. In addition, the invention provides methods of stably expressing a selectable marker in a cell, comprising introducing a MAC containing the selectable marker into the cell. The invention also provides a cell containing a MAC expressing an exogenous nucleic acid sequence and a transgenic mammal expressing a selectable marker.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 1998:19593 USPATFULL  
 TITLE: Mammalian artificial chromosomes and methods of using same  
 INVENTOR(S): Scheffler, Immo E., Del Mar, CA, United States  
 PATENT ASSIGNEE(S): The Regents of the University of California, San Diego, Alameda, CA, United States (U.S. corporation)

|                     | NUMBER         | KIND | DATE         |
|---------------------|----------------|------|--------------|
| PATENT INFORMATION: | US 5721118     |      | 19980224     |
| APPLICATION INFO.:  | US 1996-741406 |      | 19961029 (8) |

|                       | NUMBER                                 | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 1995-39256P                         | 19951031 (60) |
| DOCUMENT TYPE:        | Utility                                |               |
| FILE SEGMENT:         | Granted                                |               |
| PRIMARY EXAMINER:     | Chambers, Jasmine C.                   |               |
| ASSISTANT EXAMINER:   | Schmuck, Jill D.                       |               |
| LEGAL REPRESENTATIVE: | Campbell & Flores LLP                  |               |
| NUMBER OF CLAIMS:     | 17                                     |               |
| EXEMPLARY CLAIM:      | 2,7,17                                 |               |
| NUMBER OF DRAWINGS:   | 6 Drawing Figure(s); 3 Drawing Page(s) |               |
| LINE COUNT:           | 1797                                   |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L7 ANSWER 26 OF 27 EMBASE COPYRIGHT 2004 ELSEVIER INC. ALL RIGHTS RESERVED.  
on STN

TI High-level heterologous gene expression in *Saccharomyces cerevisiae* from a stable 2µm plasmid system.

AB The best candidate for a high-copy-number and mitotic **stability** expression system in yeast is the endogenous 2µm plasmid. Nevertheless, derivatives of the 2µm plasmid typically exhibit lower copy numbers and require selection for adequate maintenance within cells. We report the construction and utilization of an efficient heterologous gene expression system containing a 4.5-kb inducible expression cassette inserted into the 2µm plasmid and selected in cells utilizing a carrier plasmid which is subsequently lost via **FRT/Flp recombination**. The non-selectable 2µm plasmid, containing the cassette, was found to be stably maintained in cells, without selection, at high copy number. The dynamics of resolution and partitioning of this plasmid were analyzed during the course of 50 generations of growth under non-selective conditions. The heterologous lacZ reporter gene coding for β-galactosidase (βGal) is driven by the hybrid, galactose-inducible promoter GAL10::pMFα1. Upon induction, βGal was secreted into the periplasm and culture supernatant at levels which could be detected directly from Coomassie blue-stained SDS-PAGE. Furthermore, plasmid-containing cells could be maintained directly on rich YPD medium and identified either by utilizing XGal or by observing inhibition of colony growth on YPGal solid medium. The cassette was designed for direct, high-level, inducible expression of cloned genes downstream from the MFα1 signal sequence, with or without a C-terminal lacZ fusion. This vector represents the first demonstration of a non-selectable, mitotically stable, episomal plasmid system capable of expressing recombinant proteins at high levels. By supplanting the need for synthetic medium, this system could provide both an efficient and cost-effective means of generating recombinant protein at either the laboratory or large-scale level.

ACCESSION NUMBER: 93310911 EMBASE  
DOCUMENT NUMBER: 1993310911  
TITLE: High-level heterologous gene expression in *Saccharomyces cerevisiae* from a stable 2µm plasmid system.  
AUTHOR: Ludwig D.L.; Ugolini S.; Bruschi C.V.  
CORPORATE SOURCE: Microbiology Department, Internat. Ct. Gen.  
Eng./Biotechnol., Padriciano 99, I-34012 Trieste, Italy  
SOURCE: Gene, (1993) 132/1 (33-40).  
ISSN: 0378-1119 CODEN: GENED6  
COUNTRY: Netherlands  
DOCUMENT TYPE: Journal; Article  
FILE SEGMENT: 004 Microbiology  
LANGUAGE: English



SUMMARY LANGUAGE: English

L7 ANSWER 27 OF 27 BIOSIS COPYRIGHT 2004 BIOLOGICAL ABSTRACTS INC. on STN  
TI High-level heterologous gene expression in *Saccharomyces cerevisiae* from a  
stable 2- $\mu$ -m plasmid system.  
AB The best candidate for a high-copy-number and mitotic **stability**  
expression system in yeast is the endogenous 2- $\mu$ -m plasmid.  
Nevertheless, derivatives of the 2- $\mu$ -m plasmid typically exhibit lower  
copy numbers and require selection for adequate maintenance within cells.  
We report the construction and utilization of an efficient heterologous  
gene expression system containing a 4.5-kb inducible expression cassette  
inserted into the 2- $\mu$ -m plasmid and selected in cells utilizing a carrier  
plasmid which is subsequently lost via **FRT/Flp**  
**recombination**. The non-selectable 2- $\mu$ -m plasmid, containing the  
cassette, was found to be stably maintained in cells, without selection,  
at high copy number. The dynamics of resolution and partitioning of this  
plasmid were analyzed during the course of 50 generations of growth under  
non-selective conditions. The heterologous lacZ reporter gene coding for  
beta-galactosidase (beta-Gal) is driven by the hybrid, galactose-inducible  
promoter GAL10::pMF-alpha-1. Upon induction, beta-Gal was secreted into  
the periplasm and culture supernatant at levels which could be detected  
directly from Coomassie blue-stained SDS-PAGE. Furthermore,  
plasmid-containing cells could be maintained directly on rich YPD medium  
and identified either by utilizing XGal or by observing inhibition of  
colony growth on YPGal solid medium. The cassette was designed for  
direct, high-level, inducible expression of cloned genes downstream from  
the MF-alpha-1 signal sequence, with or without a C-terminal lacZ fusion.  
This vector represents the first demonstration of a non-selectable,  
mitotically stable, episomal plasmid system capable of expressing  
recombinant proteins at high levels. By supplanting the need for  
synthetic medium, this system could provide both an efficient and  
cost-effective means of generating recombinant protein at either the  
laboratory or large-scale level.

ACCESSION NUMBER: 1993:585676 BIOSIS  
DOCUMENT NUMBER: PREV199497005046  
TITLE: High-level heterologous gene expression in *Saccharomyces*  
*cerevisiae* from a stable 2- $\mu$ -m plasmid system.  
AUTHOR(S): Ludwig, Dale L.; Ugolini, Simone; Bruschi, Carlo V.  
[Reprint author]  
CORPORATE SOURCE: Microbiol. Dep., Int. Centre Genetic Eng. and Biotechnol.,  
Padriciano 99, I-34012 Trieste, Italy  
SOURCE: Gene (Amsterdam), (1993) Vol. 132, No. 1, pp. 33-40.  
CODEN: GENED6. ISSN: 0378-1119.  
DOCUMENT TYPE: Article  
LANGUAGE: English  
ENTRY DATE: Entered STN: 28 Dec 1993  
Last Updated on STN: 28 Dec 1993

=> s his

L8 583163 HIS

=> d his

(FILE 'HOME' ENTERED AT 17:55:13 ON 29 MAR 2004)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, FSTA, CEN, BIOSIS'  
ENTERED AT 17:55:41 ON 29 MAR 2004

L1 0 S FRT/FLP  
L2 6180 S FRT OR FLP  
L3 1238 S CRE LOX  
L4 0 S L2 AND STABLE RECOMBINATION  
L5 96 S FRT () FLP  
L6 82 S L5 AND RECOMBINATION

L7 27 S L6 AND STABILITY  
L8 583163 S HIS

=> s l7 and ARS  
L9 0 L7 AND ARS

=> s autonomous replicating sequence  
4 FILES SEARCHED...  
L10 217 AUTONOMOUS REPLICATING SEQUENCE

=> s l10 and l7  
L11 0 L10 AND L7

=> s "1400 LNH-ST"  
L12 0 "1400 LNH-ST"

=> s plasmid and "1400"  
L13 5601 PLASMID AND "1400"

=> s XR or XD or XK  
L14 16569 XR OR XD OR XK

=> s l14 and l7  
L15 0 L14 AND L7

=> d his

(FILE 'HOME' ENTERED AT 17:55:13 ON 29 MAR 2004)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, FSTA, CEN, BIOSIS'  
ENTERED AT 17:55:41 ON 29 MAR 2004

L1 0 S FRT/FLP  
L2 6180 S FRT OR FLP  
L3 1238 S CRE LOX  
L4 0 S L2 AND STABLE RECOMBINATION  
L5 96 S FRT () FLP  
L6 82 S L5 AND RECOMBINATION  
L7 27 S L6 AND STABILITY  
L8 583163 S HIS  
L9 0 S L7 AND ARS  
L10 217 S AUTONOMOUS REPLICATING SEQUENCE  
L11 0 S L10 AND L7  
L12 0 S "1400 LNH-ST"  
L13 5601 S PLASMID AND "1400"  
L14 16569 S XR OR XD OR XK  
L15 0 S L14 AND L7

=> s l3 and l10  
L16 7 L3 AND L10

=> d l16 ti abs ibib tot

L16 ANSWER 1 OF 7 USPATFULL on STN  
TI Methods for isolating centromere DNA  
AB The invention provides efficient methods for the isolation of  
centromeres from potentially any organism. The methods represents an  
advance over the prior art in that costly and labor intensive mapping  
programs are not required. Using the technique, methylated centromere  
DNA may be isolated from potentially any centromere in an organism. The  
technique is amenable to mass screenings employing use of arrays  
comprising libraries of DNA from a target species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.  
ACCESSION NUMBER: 2004:31144 USPATFULL

TITLE: Methods for isolating centromere DNA  
INVENTOR(S): Luo, Song, Chicago, IL, UNITED STATES  
Copenhaver, Gregory, Oak Park, IL, UNITED STATES  
Keith, Kevin, Chicago, IL, UNITED STATES  
Preuss, Daphne, Chicago, IL, UNITED STATES

|                       | NUMBER  | KIND | DATE          |
|-----------------------|---|------|---------------|
| PATENT INFORMATION:   | US 2004023282   | A1   | 20040205      |
| APPLICATION INFO.:    | US 2003-620924  | A1   | 20030716 (10) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 2001-888220, filed on 22 Jun 2001, GRANTED, Pat. No. US 6649347 |      |               |

|  | NUMBER   | DATE          |
|--|--|---------------|
| PRIORITY INFORMATION:                      | US 2000-228793P  | 20000623 (60) |
| DOCUMENT TYPE:                             | Utility  |               |
| FILE SEGMENT:                              | APPLICATION  |               |
| LEGAL REPRESENTATIVE:                      | BELL, BOYD & LLOYD LLC, P.O. Box 1135, Chicago, IL, 60690-1135 |               |
| NUMBER OF CLAIMS:                          | 119  |               |
| EXEMPLARY CLAIM:                           | 1  |               |
| NUMBER OF DRAWINGS:                        | 40 Drawing Page(s)   |               |
| LINE COUNT:                                | 4102   |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |

L16 ANSWER 2 OF 7 USPATFULL on STN

TI Methods for generating or increasing revenues from crops  
AB The present invention provides methods of doing business and providing services. For example, methods of increasing the revenue of crops are provided. To this end, the method includes the use of a nucleic acid sequences of plant centromeres. This will permit construction of stably inherited recombinant DNA constructs and mini chromosomes which can serve as vectors for the construction of transgenic plant and animal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:189578 USPATFULL  
TITLE: Methods for generating or increasing revenues from crops  
INVENTOR(S): Copenhaver, Gregory, Chapel Hill, NC, UNITED STATES  
Keith, Kevin, Chicago, IL, UNITED STATES  
Preuss, Daphne, Chicago, IL, UNITED STATES

|                       | NUMBER  | KIND | DATE          |
|-----------------------|---|------|---------------|
| PATENT INFORMATION:   | US 2003131372   | A1   | 20030710      |
| APPLICATION INFO.:    | US 2002-170944  | A1   | 20020612 (10) |
| RELATED APPLN. INFO.: | Continuation-in-part of Ser. No. US 2000-553231, filed on 19 Apr 2000, PENDING Continuation of Ser. No. US 1998-90051, filed on 3 Jun 1998, GRANTED, Pat. No. US 6156953 Continuation-in-part of Ser. No. US 2000-531120, filed on 17 Mar 2000, PENDING |      |               |

|                       | NUMBER          | DATE          |
|-----------------------|-----------------|---------------|
| PRIORITY INFORMATION: | US 1997-48451P  | 19970603 (60) |
|                       | US 1998-73741P  | 19980205 (60) |
|                       | US 1999-125219P | 19990318 (60) |
|                       | US 1999-127409P | 19990401 (60) |
|                       | US 1999-134770P | 19990518 (60) |
|                       | US 1999-153584P | 19990913 (60) |
|                       | US 1999-154603P | 19990917 (60) |
|                       | US 1999-172493P | 19991216 (60) |

DOCUMENT TYPE: Utility  
FILE SEGMENT: APPLICATION  
LEGAL REPRESENTATIVE: Bell, Boyd & Lloyd LLC, P.O. Box 1135, Chicago, IL,  
60690-1135  
NUMBER OF CLAIMS: 91  
EXEMPLARY CLAIM: 1  
NUMBER OF DRAWINGS: 46 Drawing Page(s)  
LINE COUNT: 4575  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 3 OF 7 USPATFULL on STN  
TI Plant centromere compositions  
AB The present invention provides for the nucleic acid sequences of plant centromeres. This will permit construction of stably inherited recombinant DNA constructs and minichromosomes which can serve as vectors for the construction of transgenic plant and animal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:180731 USPATFULL  
TITLE: Plant centromere compositions  
INVENTOR(S): Mach, Jennifer, Chicago, IL, UNITED STATES  
Zieler, Helge, Chicago, IL, UNITED STATES  
Jin, RongGuan, Chicago, IL, UNITED STATES  
Keith, Kevin, Chicago, IL, UNITED STATES  
Copenhaver, Gregory, Chapel Hill, NC, UNITED STATES  
Preuss, Daphne, Chicago, IL, UNITED STATES

|                       | NUMBER  | KIND | DATE          |
|-----------------------|---|------|---------------|
| PATENT INFORMATION:   | US 2003124561   | A1   | 20030703      |
| APPLICATION INFO.:    | US 2002-170912  | A1   | 20020612 (10) |
| RELATED APPLN. INFO.: | Continuation-in-part of Ser. No. US 2000-553231, filed on 19 Apr 2000, PENDING Continuation of Ser. No. US 1998-90051, filed on 3 Jun 1998, GRANTED, Pat. No. US 6156953 Continuation-in-part of Ser. No. US 2000-531120, filed on 17 Mar 2000, PENDING |      |               |

|                       | NUMBER          | DATE          |
|-----------------------|-----------------|---------------|
| PRIORITY INFORMATION: | US 1997-48451P  | 19970603 (60) |
|                       | US 1998-73741P  | 19980205 (60) |
|                       | US 1999-125219P | 19990318 (60) |
|                       | US 1999-127409P | 19990401 (60) |
|                       | US 1999-134770P | 19990518 (60) |
|                       | US 1999-153584P | 19990913 (60) |
|                       | US 1999-154603P | 19990917 (60) |
|                       | US 1999-172493P | 19991216 (60) |

DOCUMENT TYPE: Utility  
FILE SEGMENT: APPLICATION  
LEGAL REPRESENTATIVE: BELL, BOYD & LLOYD, LLC, PO BOX 1135, CHICAGO, IL,  
60690-1135  
NUMBER OF CLAIMS: 127  
EXEMPLARY CLAIM: 1  
NUMBER OF DRAWINGS: 46 Drawing Page(s)  
LINE COUNT: 4478  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 4 OF 7 USPATFULL on STN  
TI Methods for isolating centromere DNA  
AB The invention provides efficient methods for the isolation of centromeres from potentially any organism. The methods represents an advance over the prior art in that costly and labor intensive mapping programs are not required. Using the technique, methylated centromere DNA may be isolated from potentially any centromere in an organism. The

technique is amenable to mass screenings employing use of arrays comprising libraries of DNA from a target species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:227900 USPATFULL  
TITLE: Methods for isolating centromere DNA  
INVENTOR(S): Luo, Song, Chicago, IL, UNITED STATES  
Copenhaver, Gregory, Oak Park, IL, UNITED STATES  
Keith, Kevin, Chicago, IL, UNITED STATES  
Preuss, Daphne, Chicago, IL, UNITED STATES  
PATENT ASSIGNEE(S): University of Chicago (U.S. corporation)

|                     | NUMBER         | KIND | DATE         |
|---------------------|----------------|------|--------------|
| PATENT INFORMATION: | US 2002123053  | A1   | 20020905     |
|                     | US 6649347     | B2   | 20031118     |
| APPLICATION INFO.:  | US 2001-888220 | A1   | 20010622 (9) |

|                       | NUMBER  | DATE          |
|-----------------------|---|---------------|
| PRIORITY INFORMATION: | US 2000-228793P   | 20000623 (60) |
| DOCUMENT TYPE:        | Utility   |               |
| FILE SEGMENT:         | APPLICATION   |               |
| LEGAL REPRESENTATIVE: | BELL, BOYD & LLOYD, LLC, PO BOX 1135, CHICAGO, IL, 60690-1135 |               |
| NUMBER OF CLAIMS:     | 119   |               |
| EXEMPLARY CLAIM:      | 1   |               |
| NUMBER OF DRAWINGS:   | 40 Drawing Page(s)  |               |
| LINE COUNT:           | 4078  |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 5 OF 7 USPATFULL on STN

TI Telomerase compositions and methods  
AB Disclosed are various methods, compositions and screening assays connected with telomerase, including genes encoding the template RNA of *S. cerevisiae* telomerase and various telomerase-associated polypeptides.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:108815 USPATFULL  
TITLE: Telomerase compositions and methods  
INVENTOR(S): Gottschling, Daniel E., Chicago, IL, United States  
Singer, Miriam S., Chicago, IL, United States  
PATENT ASSIGNEE(S): Arch Development, Chicago, IL, United States (U.S. corporation)

|                       | NUMBER  | KIND | DATE         |
|-----------------------|---|------|--------------|
| PATENT INFORMATION:   | US 6387619  | B1   | 20020514     |
| APPLICATION INFO.:    | US 1999-345294  |      | 19990630 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1997-938534, filed on 26 Sep 1997, now patented, Pat. No. US 5916752 Division of Ser. No. US 1995-431080, filed on 28 Apr 1995, now patented, Pat. No. US 5698686 Division of Ser. No. US 345294 Continuation-in-part of Ser. No. US 1994-326781, filed on 20 Oct 1994, now abandoned |      |              |
| DOCUMENT TYPE:        | Utility   |      |              |
| FILE SEGMENT:         | GRANTED   |      |              |
| PRIMARY EXAMINER:     | Fredman, Jeffrey  |      |              |
| LEGAL REPRESENTATIVE: | Fulbright & Jaworski, LLP   |      |              |
| NUMBER OF CLAIMS:     | 10  |      |              |
| EXEMPLARY CLAIM:      | 1   |      |              |
| NUMBER OF DRAWINGS:   | 15 Drawing Figure(s); 11 Drawing Page(s)  |      |              |
| LINE COUNT:           | 6648  |      |              |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 6 OF 7 USPATFULL on STN  
TI Telomerase screening methods  
AB Disclosed are various methods, compositions and screening assays connected with telomerase, including genes encoding the template RNA of *S. cerevisiae* telomerase and various telomerase-associated polypeptides.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 1999:72446 USPATFULL  
TITLE: Telomerase screening methods  
INVENTOR(S): Gottschling, Daniel E., Chicago, IL, United States  
Singer, Miriam S., Chicago, IL, United States  
PATENT ASSIGNEE(S): Arch Development Corporation, Chicago, IL, United States (U.S. corporation)

|                       | NUMBER   | KIND | DATE         |
|-----------------------|--|------|--------------|
| PATENT INFORMATION:   | US 5916752   |      | 19990629     |
| APPLICATION INFO.:    | US 1997-938534   |      | 19970926 (8) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1995-431080, filed on 28 Apr 1995, now patented, Pat. No. US 5698686 which is a continuation-in-part of Ser. No. US 1994-326781, filed on 20 Oct 1994, now abandoned |      |              |
| DOCUMENT TYPE:        | Utility  |      |              |
| FILE SEGMENT:         | Granted  |      |              |
| PRIMARY EXAMINER:     | Fredman, Jeffrey   |      |              |
| LEGAL REPRESENTATIVE: | Arnold, White & Durkee   |      |              |
| NUMBER OF CLAIMS:     | 56   |      |              |
| EXEMPLARY CLAIM:      | 1  |      |              |
| NUMBER OF DRAWINGS:   | 15 Drawing Figure(s); 15 Drawing Page(s)   |      |              |
| LINE COUNT:           | 7780   |      |              |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L16 ANSWER 7 OF 7 USPATFULL on STN  
TI Yeast telomerase compositions  
AB Disclosed are various methods, compositions and screening assays connected with telomerase, including genes encoding the template RNA of *S. cerevisiae* telomerase and various telomerase-associated polypeptides.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 97:118172 USPATFULL  
TITLE: Yeast telomerase compositions  
INVENTOR(S): Gottschling, Daniel E., Chicago, IL, United States  
Singer, Miriam S., Chicago, IL, United States  
PATENT ASSIGNEE(S): Arch Development Corporation, Chicago, IL, United States (U.S. corporation)

|                       | NUMBER   | KIND | DATE         |
|-----------------------|--|------|--------------|
| PATENT INFORMATION:   | US 5698686   |      | 19971216     |
| APPLICATION INFO.:    | US 1995-431080   |      | 19950428 (8) |
| RELATED APPLN. INFO.: | Continuation-in-part of Ser. No. US 1994-326781, filed on 20 Oct 1994, now abandoned |      |              |
| DOCUMENT TYPE:        | Utility  |      |              |
| FILE SEGMENT:         | Granted  |      |              |
| PRIMARY EXAMINER:     | Jones, W. Gary   |      |              |
| ASSISTANT EXAMINER:   | Fredman, Jeffrey   |      |              |
| LEGAL REPRESENTATIVE: | Arnold, White & Durkee   |      |              |
| NUMBER OF CLAIMS:     | 71   |      |              |
| EXEMPLARY CLAIM:      | 1  |      |              |
| NUMBER OF DRAWINGS:   | 15 Drawing Figure(s); 15 Drawing Page(s)   |      |              |
| LINE COUNT:           | 7319   |      |              |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

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(FILE 'HOME' ENTERED AT 17:55:13 ON 29 MAR 2004)

FILE 'MEDLINE, USPATFULL, DGENE, EMBASE, WPIDS, FSTA, CEN, BIOSIS'  
ENTERED AT 17:55:41 ON 29 MAR 2004

L1 0 S FRT/FLP  
L2 6180 S FRT OR FLP  
L3 1238 S CRE LOX  
L4 0 S L2 AND STABLE RECOMBINATION  
L5 96 S FRT () FLP  
L6 82 S L5 AND RECOMBINATION  
L7 27 S L6 AND STABILITY  
L8 583163 S HIS  
L9 0 S L7 AND ARS  
L10 217 S AUTONOMOUS REPLICATING SEQUENCE  
L11 0 S L10 AND L7  
L12 0 S "1400 LNH-ST"  
L13 5601 S PLASMID AND "1400"  
L14 16569 S XR OR XD OR XK  
L15 0 S L14 AND L7  
L16 7 S L3 AND L10

=> s l2 and l10

L17 8 L2 AND L10

=> d l17 ti abs ibib tot

L17 ANSWER 1 OF 8 USPATFULL on STN

TI Methods for isolating centromere DNA

AB The invention provides efficient methods for the isolation of centromeres from potentially any organism. The methods represents an advance over the prior art in that costly and labor intensive mapping programs are not required. Using the technique, methylated centromere DNA may be isolated from potentially any centromere in an organism. The technique is amenable to mass screenings employing use of arrays comprising libraries of DNA from a target species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2004:31144 USPATFULL

TITLE: Methods for isolating centromere DNA

INVENTOR(S): Luo, Song, Chicago, IL, UNITED STATES

Copenhaver, Gregory, Oak Park, IL, UNITED STATES

Keith, Kevin, Chicago, IL, UNITED STATES

Preuss, Daphne, Chicago, IL, UNITED STATES

|                       | NUMBER  | KIND | DATE          |
|-----------------------|---|------|---------------|
| PATENT INFORMATION:   | US 2004023282   | A1   | 20040205      |
| APPLICATION INFO.:    | US 2003-620924  | A1   | 20030716 (10) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 2001-888220, filed on 22 Jun 2001, GRANTED, Pat. No. US 6649347 |      |               |

|                       | NUMBER   | DATE          |
|-----------------------|--|---------------|
| PRIORITY INFORMATION: | US 2000-228793P  | 20000623 (60) |
| DOCUMENT TYPE:        | Utility  |               |
| FILE SEGMENT:         | APPLICATION  |               |
| LEGAL REPRESENTATIVE: | BELL, BOYD & LLOYD LLC, P.O. Box 1135, Chicago, IL, 60690-1135 |               |
| NUMBER OF CLAIMS:     | 119  |               |
| EXEMPLARY CLAIM:      | 1  |               |
| NUMBER OF DRAWINGS:   | 40 Drawing Page(s)   |               |

LINE COUNT: 4102  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 2 OF 8 USPATFULL on STN

TI Methods for generating or increasing revenues from crops  
AB The present invention provides methods of doing business and providing services. For example, methods of increasing the revenue of crops are provided. To this end, the method includes the use of a nucleic acid sequences of plant centromeres. This will permit construction of stably inherited recombinant DNA constructs and mini chromosomes which can serve as vectors for the construction of transgenic plant and animal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:189578 USPATFULL  
TITLE: Methods for generating or increasing revenues from crops  
INVENTOR(S): Copenhagen, Gregory, Chapel Hill, NC, UNITED STATES  
Keith, Kevin, Chicago, IL, UNITED STATES  
Preuss, Daphne, Chicago, IL, UNITED STATES

|                       | NUMBER  | KIND | DATE          |
|-----------------------|---|------|---------------|
| PATENT INFORMATION:   | US 2003131372   | A1   | 20030710      |
| APPLICATION INFO.:    | US 2002-170944  | A1   | 20020612 (10) |
| RELATED APPLN. INFO.: | Continuation-in-part of Ser. No. US 2000-553231, filed on 19 Apr 2000, PENDING Continuation of Ser. No. US 1998-90051, filed on 3 Jun 1998, GRANTED, Pat. No. US 6156953 Continuation-in-part of Ser. No. US 2000-531120, filed on 17 Mar 2000, PENDING |      |               |

|                       | NUMBER          | DATE          |
|-----------------------|-----------------|---------------|
| PRIORITY INFORMATION: | US 1997-48451P  | 19970603 (60) |
|                       | US 1998-73741P  | 19980205 (60) |
|                       | US 1999-125219P | 19990318 (60) |
|                       | US 1999-127409P | 19990401 (60) |
|                       | US 1999-134770P | 19990518 (60) |
|                       | US 1999-153584P | 19990913 (60) |
|                       | US 1999-154603P | 19990917 (60) |
|                       | US 1999-172493P | 19991216 (60) |

DOCUMENT TYPE: Utility  
FILE SEGMENT: APPLICATION  
LEGAL REPRESENTATIVE: Bell, Boyd & Lloyd LLC, P.O. Box 1135, Chicago, IL, 60690-1135

NUMBER OF CLAIMS: 91  
EXEMPLARY CLAIM: 1  
NUMBER OF DRAWINGS: 46 Drawing Page(s)  
LINE COUNT: 4575  
CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 3 OF 8 USPATFULL on STN

TI Plant centromere compositions  
AB The present invention provides for the nucleic acid sequences of plant centromeres. This will permit construction of stably inherited recombinant DNA constructs and minichromosomes which can serve as vectors for the construction of transgenic plant and animal cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:180731 USPATFULL  
TITLE: Plant centromere compositions  
INVENTOR(S): Mach, Jennifer, Chicago, IL, UNITED STATES  
Zieler, Helge, Chicago, IL, UNITED STATES  
Jin, RongGuan, Chicago, IL, UNITED STATES



Keith, Kevin, Chicago, IL, UNITED STATES  
Copenhaver, Gregory, Chapel Hill, NC, UNITED STATES  
Preuss, Daphne, Chicago, IL, UNITED STATES

|                       | NUMBER  | KIND | DATE          |
|-----------------------|---|------|---------------|
| PATENT INFORMATION:   | US 2003124561   | A1   | 20030703      |
| APPLICATION INFO.:    | US 2002-170912  | A1   | 20020612 (10) |
| RELATED APPLN. INFO.: | Continuation-in-part of Ser. No. US 2000-553231, filed on 19 Apr 2000, PENDING Continuation of Ser. No. US 1998-90051, filed on 3 Jun 1998, GRANTED, Pat. No. US 6156953 Continuation-in-part of Ser. No. US 2000-531120, filed on 17 Mar 2000, PENDING |      |               |

|  | NUMBER  | DATE          |
|--|---|---------------|
| PRIORITY INFORMATION:                      | US 1997-48451P  | 19970603 (60) |
|  | US 1998-73741P  | 19980205 (60) |
|  | US 1999-125219P   | 19990318 (60) |
|  | US 1999-127409P   | 19990401 (60) |
|  | US 1999-134770P   | 19990518 (60) |
|  | US 1999-153584P   | 19990913 (60) |
|  | US 1999-154603P   | 19990917 (60) |
|  | US 1999-172493P   | 19991216 (60) |
| DOCUMENT TYPE:                             | Utility   |               |
| FILE SEGMENT:                              | APPLICATION   |               |
| LEGAL REPRESENTATIVE:                      | BELL, BOYD & LLOYD, LLC, PO BOX 1135, CHICAGO, IL, 60690-1135 |               |
| NUMBER OF CLAIMS:                          | 127   |               |
| EXEMPLARY CLAIM:                           | 1   |               |
| NUMBER OF DRAWINGS:                        | 46 Drawing Page(s)  |               |
| LINE COUNT:                                | 4478  |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |   |               |

L17 ANSWER 4 OF 8 USPATFULL on STN

TI Rapid creation of gene targeting vectors using homologous recombination in yeast

AB The present invention provides methods of preparing gene targeted mammalian cells having a targeted gene mutation methods of making gene targeted mice, and gene targeting vectors that are useful in these methods.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2003:134098 USPATFULL  
TITLE: Rapid creation of gene targeting vectors using homologous recombination in yeast  
INVENTOR(S): Fisher, Katherine E., Old Lyme, CT, UNITED STATES  
Reaume, Andrew G., Waterford, CT, UNITED STATES

|  | NUMBER  | KIND | DATE         |
|--|---|------|--------------|
| PATENT INFORMATION:                        | US 2003092183   | A1   | 20030515     |
| APPLICATION INFO.:                         | US 2001-961163  | A1   | 20010921 (9) |
| DOCUMENT TYPE:                             | Utility   |      |              |
| FILE SEGMENT:                              | APPLICATION   |      |              |
| LEGAL REPRESENTATIVE:                      | Gregg C. Benson, Pfizer Inc., Patent Department, MS 4159, Eastern Point Road, Groton, CT, 06340 |      |              |
| NUMBER OF CLAIMS:                          | 20  |      |              |
| EXEMPLARY CLAIM:                           | 1   |      |              |
| NUMBER OF DRAWINGS:                        | 2 Drawing Page(s)   |      |              |
| LINE COUNT:                                | 1249  |      |              |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |   |      |              |

L17 ANSWER 5 OF 8 USPATFULL on STN

TI Methods for isolating centromere DNA  
AB The invention provides efficient methods for the isolation of centromeres from potentially any organism. The methods represents an advance over the prior art in that costly and labor intensive mapping programs are not required. Using the technique, methylated centromere DNA may be isolated from potentially any centromere in an organism. The technique is amenable to mass screenings employing use of arrays comprising libraries of DNA from a target species.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:227900 USPATFULL  
TITLE: Methods for isolating centromere DNA  
INVENTOR(S): Luo, Song, Chicago, IL, UNITED STATES  
Copenhaver, Gregory, Oak Park, IL, UNITED STATES  
Keith, Kevin, Chicago, IL, UNITED STATES  
Preuss, Daphne, Chicago, IL, UNITED STATES  
PATENT ASSIGNEE(S): University of Chicago (U.S. corporation)

|                     | NUMBER         | KIND | DATE         |
|---------------------|----------------|------|--------------|
| PATENT INFORMATION: | US 2002123053  | A1   | 20020905     |
|                     | US 6649347     | B2   | 20031118     |
| APPLICATION INFO.:  | US 2001-888220 | A1   | 20010622 (9) |

|                       | NUMBER  | DATE          |
|-----------------------|---|---------------|
| PRIORITY INFORMATION: | US 2000-228793P   | 20000623 (60) |
| DOCUMENT TYPE:        | Utility   |               |
| FILE SEGMENT:         | APPLICATION   |               |
| LEGAL REPRESENTATIVE: | BELL, BOYD & LLOYD, LLC, PO BOX 1135, CHICAGO, IL, 60690-1135 |               |
| NUMBER OF CLAIMS:     | 119   |               |
| EXEMPLARY CLAIM:      | 1   |               |
| NUMBER OF DRAWINGS:   | 40 Drawing Page(s)  |               |
| LINE COUNT:           | 4078  |               |

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

L17 ANSWER 6 OF 8 USPATFULL on STN

TI Methods for the production of gelatin and full-length triple helical collagen in recombinant cells  
AB Methods are disclosed for simplified recombinant production of fibrillar collagens. DNAs encoding fibrillar collagen monomers lacking the N propeptide, the C propeptide, or both propeptides are introduced into recombinant host cells and expressed. Trimeric collagen is recovered from the recombinant host cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:194714 USPATFULL  
TITLE: Methods for the production of gelatin and full-length triple helical collagen in recombinant cells  
INVENTOR(S): Olsen, David R., Menlo Park, CA, United States  
Chang, Robert, Hillsborough, CA, United States  
McMullin, Hugh, Menlo Park, CA, United States  
Hitzeman, Ronald A., Pacifica, CA, United States  
Chisholm, George, San Mateo, CA, United States  
PATENT ASSIGNEE(S): Cohesion Technologies, Inc., Palo Alto, CA, United States (U.S. corporation)  
Genotypes, Inc., Pacifica, CA, United States (U.S. corporation)

|                     | NUMBER         | KIND | DATE         |
|---------------------|----------------|------|--------------|
| PATENT INFORMATION: | US 6428978     | B1   | 20020806     |
| APPLICATION INFO.:  | US 1999-289578 |      | 19990409 (9) |

|  | NUMBER                                   | DATE          |
|--|--|---------------|
|  | -----                                    | -----         |
| PRIORITY INFORMATION:                      | US 1998-84828P                           | 19980508 (60) |
| DOCUMENT TYPE:                             | Utility                                  |               |
| FILE SEGMENT:                              | GRANTED                                  |               |
| PRIMARY EXAMINER:                          | Whisenant, Ethan C.                      |               |
| LEGAL REPRESENTATIVE:                      | Osman, Richard Aron                      |               |
| NUMBER OF CLAIMS:                          | 31                                       |               |
| EXEMPLARY CLAIM:                           | 1  |               |
| NUMBER OF DRAWINGS:                        | 14 Drawing Figure(s); 14 Drawing Page(s) |               |
| LINE COUNT:                                | 1945                                     |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |

L17 ANSWER 7 OF 8 USPATFULL on STN

TI Recombinant gelatin and full-length triple helical collagen  
 AB Methods are disclosed for simplified recombinant production of fibrillar collagens. DNAs encoding fibrillar collagen monomers lacking the N propeptide, the C propeptide, or both propeptides are introduced into recombinant host cells and expressed. Trimeric collagen is recovered from the recombinant host cells.

CAS INDEXING IS AVAILABLE FOR THIS PATENT.

ACCESSION NUMBER: 2002:160549 USPATFULL  
 TITLE: Recombinant gelatin and full-length triple helical collagen  
 INVENTOR(S): Olsen, David R., Menlo Park, CA, United States  
 Chang, Robert, Hillsborough, CA, United States  
 McMullin, Hugh, Menlo Park, CA, United States  
 Hitzeman, Ronald A., Pacifica, CA, United States  
 Chisholm, George, San Mateo, CA, United States  
 PATENT ASSIGNEE(S): Cohesion Technologies, Inc., Palo Alto, CA, United States (U.S. corporation)  
 Genotypes, Inc., Pacifica, CA, United States (U.S. corporation)

|                       | NUMBER   | KIND  | DATE         |
|-----------------------|--|-------|--------------|
|                       | -----  | ----- | -----        |
| PATENT INFORMATION:   | US 6413742   | B1    | 20020702     |
| APPLICATION INFO.:    | US 2000-585887   |       | 20000531 (9) |
| RELATED APPLN. INFO.: | Division of Ser. No. US 1999-289578, filed on 9 Apr 1999 |       |              |

|  | NUMBER                                   | DATE          |
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|  | -----                                    | -----         |
| PRIORITY INFORMATION:                      | US 1998-84828P                           | 19980508 (60) |
| DOCUMENT TYPE:                             | Utility                                  |               |
| FILE SEGMENT:                              | GRANTED                                  |               |
| PRIMARY EXAMINER:                          | Whisenant, Ethan C.                      |               |
| LEGAL REPRESENTATIVE:                      | Osman, Richard Aron                      |               |
| NUMBER OF CLAIMS:                          | 29                                       |               |
| EXEMPLARY CLAIM:                           | 1  |               |
| NUMBER OF DRAWINGS:                        | 14 Drawing Figure(s); 14 Drawing Page(s) |               |
| LINE COUNT:                                | 1573                                     |               |
| CAS INDEXING IS AVAILABLE FOR THIS PATENT. |  |               |

L17 ANSWER 8 OF 8 WPIDS COPYRIGHT 2004 THOMSON DERWENT on STN

TI Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells.

AN 2000-587529 [55] WPIDS

CR 1999-080832 [07]; 2000-587463 [55]; 2003-829605 [77]

AB WO 200055325 A UPAB: 20031128

NOVELTY - A recombinant DNA construct (I) comprising a plant centromere,

is new.

DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for the following:

- (1) a minichromosome vector comprising a plant centromere and telomere sequence;
- (2) a cell transformed with a recombinant DNA construct comprising a plant centromere;
- (3) a plant comprising the cell of (2);
- (4) a method of preparing a transgenic plant cell comprising contacting a starting plant cell with a recombinant DNA construct comprising a plant centromere;
- (5) a transgenic plant comprising a minichromosome vector;
- (6) a method for producing a minichromosome vector comprising:
  - (a) obtaining a first and second vector, where either comprises a selectable or screenable marker, an origin of replication, a telomere, and a plant centromere, and where the vectors comprise a site for site-specific recombination; and
  - (b) contacting the first vector with the second vector;
- (7) a method of screening a candidate centromere sequence for plant centromere activity comprising:
  - (a) obtaining an isolated nucleic acid sequence comprising a candidate centromere sequence;
  - (b) integratively transforming plant cells with the isolated nucleic acid; and
  - (c) screening for centromere activity;
- (8) a recombinant DNA construct comprising an Arabidopsis polyubiquitin 11 promoter comprising a defined 2000 bp sequence (given in the specification), or its fragments;
- (9) a recombinant DNA construct comprising an Arabidopsis 40S ribosomal protein S16 promoter comprising a defined 2000 bp sequence (given in the specification);
- (10) a recombinant DNA construct comprising an Arabidopsis polyubiquitin 11 3' regulatory sequence comprising a defined 2001 bp sequence (given in the specification); and
- (11) a recombinant DNA construct comprising an Arabidopsis 40S ribosomal protein S16 3' regulatory sequence comprising a defined 2000 bp sequence (given in the specification).

USE - The constructs are useful for producing stably inherited minichromosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.

Dwg.0/23

ACCESSION NUMBER: 2000-587529 [55] WPIDS  
CROSS REFERENCE: 1999-080832 [07]; 2000-587463 [55]; 2003-829605 [77]  
DOC. NO. CPI: C2000-175305  
TITLE: Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited minichromosomes which can serve as vectors for the construction of transgenic plant and animal cells.  
DERWENT CLASS: B04 C06 D16 P13  
INVENTOR(S): COPENHAVER, G; KEITH, K; PREUSS, D; JIN, R; MACH, J; ZIELER, H  
PATENT ASSIGNEE(S): (UYCH-N) UNIV CHICAGO; (COPE-I) COPENHAVER G; (JINR-I) JIN R; (KEIT-I) KEITH K; (MACH-I) MACH J; (PREU-I) PREUSS D; (ZIEL-I) ZIELER H  
COUNTRY COUNT: 91  
PATENT INFORMATION:

| PATENT NO | KIND | DATE | WEEK | LA | PG |
|-----------|------|------|------|----|----|
|-----------|------|------|------|----|----|

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WO 2000055325 A2 20000921 (200055)\* EN

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW NL  
OA PT SD SE SL SZ TZ UG ZW

W: AE AL AM AT AU AZ BA BB BG BR BY CA CH CN CR CU CZ DE DK DM EE ES  
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 LT LU LV MA MD MG MK MN MW MX NO NZ PL PT RO RU SD SE SG SI SK SL  
 TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW

AU 2000037649 A 20001004 (200101)  
 BR 2000009119 A 20011226 (200206)  
 EP 1165792 A2 20020102 (200209) EN  
 R: AT BE CH CY DE DK ES FI FR GB GR IE IT LI LU MC NL  
 US 2003124561 A1 20030703 (200345)

APPLICATION DETAILS:

| PATENT NO     | KIND        | APPLICATION     | DATE     |
|---------------|-------------|-----------------|----------|
| WO 2000055325 | A2          | WO 2000-US7392  | 20000317 |
| AU 2000037649 | A           | AU 2000-37649   | 20000317 |
| BR 2000009119 | A           | BR 2000-9119    | 20000317 |
|               |             | WO 2000-US7392  | 20000317 |
| EP 1165792    | A2          | EP 2000-916559  | 20000317 |
|               |             | WO 2000-US7392  | 20000317 |
| US 2003124561 | A1          | US 1997-48451P  | 19970603 |
|               | Provisional | US 1998-73741P  | 19980205 |
|               | Provisional | US 1998-90051   | 19980603 |
|               | Cont of     | US 1999-125219P | 19990318 |
|               | Provisional | US 1999-127409P | 19990401 |
|               | Provisional | US 1999-134770P | 19990518 |
|               | Provisional | US 1999-153584P | 19990913 |
|               | Provisional | US 1999-154603P | 19990917 |
|               | Provisional | US 1999-172493P | 19991216 |
|               | CIP of      | US 2000-531120  | 20000317 |
|               | CIP of      | US 2000-553231  | 20000419 |
|               |             | US 2002-170912  | 20020612 |

FILING DETAILS:

| PATENT NO     | KIND        | PATENT NO     |
|---------------|-------------|---------------|
| AU 2000037649 | A Based on  | WO 2000055325 |
| BR 2000009119 | A Based on  | WO 2000055325 |
| EP 1165792    | A2 Based on | WO 2000055325 |
| US 2003124561 | A1 Cont of  | US 6156953    |

PRIORITY APPLN. INFO: US 1999-172493P 19991216; US 1999-125219P  
 19990318; US 1999-127409P 19990401; US  
 1999-134770P 19990518; US 1999-153584P  
 19990913; US 1999-154603P 19990917; US  
 1997-48451P 19970603; US 1998-73741P  
 19980205; US 1998-90051 19980603; US  
 2000-531120 20000317; US 2000-553231  
 20000419; US 2002-170912 20020612

## Refine Search

### Search Results -

| Terms      | Documents |
|------------|-----------|
| L10 and L1 | 1         |

Database:

US Pre-Grant Publication Full-Text Database  
 US Patents Full-Text Database  
 US OCR Full-Text Database  
 EPO Abstracts Database  
 JPO Abstracts Database  
 Derwent World Patents Index  
 IBM Technical Disclosure Bulletins

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L11

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### Search History

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result set

*DB=USPT; PLUR=YES; OP=OR*

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|------------|-------------------------------------|--------|------------|
| <u>L11</u> | L10 and l1                          | 1      | <u>L11</u> |
| <u>L10</u> | autonomous replicating sequence     | 541459 | <u>L10</u> |
| <u>L9</u>  | L8 and l1                           | 1      | <u>L9</u>  |
| <u>L8</u>  | ARS                                 | 87461  | <u>L8</u>  |
| <u>L7</u>  | l1 and l4                           | 1      | <u>L7</u>  |
| <u>L6</u>  | L5 and l1                           | 1      | <u>L6</u>  |
| <u>L5</u>  | integrative plasmid                 | 37878  | <u>L5</u>  |
| <u>L4</u>  | replicative plasmid                 | 38012  | <u>L4</u>  |
| <u>L3</u>  | l2 and l1                           | 1      | <u>L3</u>  |
| <u>L2</u>  | replicative and integrative plasmid | 37405  | <u>L2</u>  |
| <u>L1</u>  | 5789210.pn.                         | 1      | <u>L1</u>  |

END OF SEARCH HISTORY

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L6: Entry 1 of 1

File: USPT

Aug 4, 1998

DOCUMENT-IDENTIFIER: US 5789210 A

**\*\* See image for Certificate of Correction \*\***

TITLE: Recombinant yeasts for effective fermentation of glucose and xylose

Drawing Description Text (4):FIG. 3 shows the genes cloned on and the restriction map of the plasmid pLSK15.Drawing Description Text (5):FIG. 4 shows the genes cloned on and the restriction map of the plasmid pUCKm10.Drawing Description Text (6):FIG. 5 shows the genes cloned on and the restriction map of the plasmid pLNH21.Drawing Description Text (10):FIG. 7 shows the genes cloned on and the restriction map of plasmid pLNH33.Drawing Description Text (13):

FIG. 9 is a schematic diagram outlining the construction of pBluescript II KS(-) containing the cloned XR, XD, and XK genes: four such plasmids were constructed: pKS(-)-KK-A\*R-KD-1; pKS(-)-KK-A\*R-KD-2; pKS(-)-KK-AR-KD-3; and pKS(-)-KK-AR-KD-4, as further described in Example 4.

Drawing Description Text (16):FIG. 12 is a schematic diagram outlining the construction of the plasmid pLNH21.Detailed Description Text (5):

The particular XR gene used in the applicants' studies herein was cloned from *P. stipitis* by Polymerase Chain Reaction (PCR) (Chen and Ho, 1993). The oligonucleotides required for the amplification of XR from the chromosomal DNA by PCR were synthesized according to the published sequence of the *P. stipitis* XR gene (Takama et al., 1991). The amplified XR was first cloned and stored into plasmid pUC19. The cloned XR was then fused to different promoters including the promoters of yeast TRP5 gene (Zalkin and Yanofsky, 1982) and yeast alcohol dehydrogenase I gene (ADCl) (Ammerer, 1983; Bennetzen and Hall, 1982).

Detailed Description Text (10):

The fusion of XR, XD, and XK to intact promoters from ADCl, PYK, GPD, etc., was carried out by cloning both the fragment containing the specific promoter and the structural gene of XR, XD, or XK on one of the Bluescript KS plasmids (Stratagene, La Jolla, Calif.), followed by the removal of the extra unwanted nucleotides by site-specific mutagenesis (Kunkel et al., 1987). The invention thus also provides several pBluescript II KS(-) (hereinafter pKS(-)) derivatives containing the cloned XD (fused to the pyruvate dehydrogenase promoter), XR (fused to the ADCl promoter), and XK (fused to the pyruvate kinase promoter). These recombinant plasmids are designated as pKS(-) KD-AR (or A\*R) -KK. Four such plasmids were constructed as outlined in FIG. 9. These plasmids have similar but not identical structures. The XR, XD, and XK (or KD-AR (or A\*R) -KK) cloned on these plasmids can be separated from the parent pKS(-) plasmid by a single XhoI restriction digestion.

Detailed Description Text (11):

The XR, XD, and XK genes fused to the proper promoters were then cloned on pLSK15 (FIG. 3) or pUCKm10 (FIG. 4). pLSK15, a derivative of pLX10-14 (Stavis and Ho, 1985), is a low copy number plasmid with a copy number of approximately 10 in yeast (*S. cerevisiae*). It contains the yeast 2.mu. replicon which enables the plasmid to be replicated autonomously in *S. cerevisiae* and closely related species. pLSK15 also contains the geneticin (kanamycin) resistance gene (Km.sup.R) and ampicillin resistance gene (Ap.sup.R and also amp.sup.r) which serve as selection markers in *S. cerevisiae* and other yeasts. pLSK15 also contains the XK gene fused to the yeast TRP-5 promoter. Thus, XR and XD genes fused to proper 5' noncoding sequences containing suitable promoters were inserted into pLSK15 to demonstrate the effect of the resulting plasmids on yeast xylose fermentation. To compare the effect of the presence of different genes on yeast xylose fermentation, a plasmid containing only XR and XD was also used to transform *S. cerevisiae* and the resulting yeast used in comparative fermentations. Results of the fermentation of xylose by un-engineered *S. cerevisiae*, yeast containing the cloned XR, XD, and XK (SC(pLNH21)), and yeast containing the cloned XR and XD but not XK (SC(pLNH13-32)) genes are shown in FIG. 6A, 6B, and 6C.

Detailed Description Text (12):

pUCKm10 (FIG. 4) is a high copy-number plasmid (i.e. plasmid with a copy number of about 50 or more) with a copy number close to 100 in *S. cerevisiae*. pUCKm10 is a pUC9 derivative containing the identical 2.mu. replicon, and the Km.sup.R, and Ap.sup.R genes present in pLSK15. These specific DNA fragments serve as the replicon and selection markers that enable the plasmid to be replicated autonomously in *S. cerevisiae* (and in related yeasts) and also enable the yeast transformants containing the plasmid to be distinguished from the untransformed host cells.

Detailed Description Text (13):

The applicants have constructed pUCKm10 based recombinant plasmids that contain the same XR, XD, and XK fused to 5' proper noncoding sequences containing suitable promoters. These vectors are designed to be useful to transform all *S. cerevisiae* strains and strains of related species. No special mutants are required to act as the recipient strains. Thus plasmids such as pLNH33 (FIG. 7), as well as pLNH21 (FIG. 5), can be used to transform industrial *S. cerevisiae* and other strains.

Detailed Description Text (14):

Yeast transformation with derivatives of either pLSK15 or pUCKm10 was carried out by electroporation generally using the the procedure described by Becker and Guarente (1991). Authentic yeast transformants containing derivatives of either pLSK15 or pUCKm10 were isolated as further described below. Km.sup.R present in the plasmids served as the primary selection marker which renders any host cells obtaining one of these plasmids resistant to a much higher concentration of geneticin present in the medium. However, some yeast cells can be induced to become resistant to the same level of geneticin of the transformants containing the plasmid. Thus, not every geneticin resistant colony is a true transformant. It has been reported that Ap.sup.R can be expressed in *S. cerevisiae* but the latter is resistant to ampicillin without the presence of Ap.sup.R. Thus, Ap.sup.R cannot serve as a selection marker for yeast plasmid-mediated transformation. Nevertheless, yeasts that contain the highly expressed Ap.sup.R will produce sufficient penicillinase and make it possible to identify colonies containing such yeasts on special solid plates by the penicillinase test (Chevallier and Aigle, 1979). The latter test has provided a technique to identify the true transformants of *S. cerevisiae* and other yeasts from the geneticin resistant colonies.

Detailed Description Text (18):

pLNH33 is a more effective plasmid than pLNH21 for xylose fermentation because it is a higher copy-number plasmid. Furthermore, the XK in pLNH33 is fused to a more



efficient promoter than the XK in pLNH21. *S. cerevisiae* has also been transformed with pLNH33, designated SC(pLNH33). Although SC(pLNH33) is much more effective in fermenting xylose or mixtures of xylose and glucose than SC(pLNH21), 1400(pLNH33) was found to be more effective in fermenting mixtures of glucose and xylose than SC(pLNH33). Thus, individual strains also affect the efficiency of fermentation. Similar to *S. cerevisiae*, the unengineered strain 1400 cannot use or ferment xylose (alone or in a mixture of glucose and xylose) as shown in FIG. 8B.

Detailed Description Text (30):

Oligonucleotides I and II were used to synthesize the intact XD gene and oligonucleotides II and III were used to synthesize the promotorless XD as shown in FIG. 10. The intact XD and the promotorless XD were first cloned in pKS(-) plasmid. The intact XR was then subcloned on pUCKm10 (FIG. 4) and the resulting plasmid pUCKm10-XD, was used to transform *S. cerevisiae* by electroporation as described in Example 5. The yeast transformants were used to assay the xylitol dehydrogenase activity to demonstrate that the cloned gene is intact and can be expressed in *S. cerevisiae*.

Detailed Description Text (34):

The promoter fragment of yeast pyruvate kinase from -910 to +23 (Burke et al., 1983) was synthesized by PCR as described in Example 1 for the synthesis of the XD gene. Both the P.sub.PK fragment and the promotorless XD were subcloned on pKS(-) plasmid and the undesired nucleotides between the P.sub.PK and the intact XD structural gene were removed by site-specific mutagenesis according to the procedure of Kunkel (Kunkel, 1987). The resulting fused gene contains -910 to -1 promoter fragments from the pyruvate kinase gene and +1 to +1963 nucleotides from the Pichia XD gene. The resulting pKS(-) plasmid containing P.sub.PK -XD (or KD) is designated pKS(-)-KD or pKD2.

Detailed Description Text (40):

Plasmid pMA56 (Ammerer, 1983) contains the yeast alcohol dehydrogenase I promoter (P.sub.ADC1). The applicants have used this promoter to modify some of the genes in their work. For example, P.sub.ADC1 has been fused to XR, and the resulting gene has been designated P.sub.ADC1 -XR or AR. Nevertheless, this P.sub.ADC1 is not intact and does not contain the -1 to -14 nucleotides of the intact ADC1 promoter (Bennetzen and Hall, 1982). The -1 to -14 region of a gene is usually very significant for controlling protein synthesis. Any gene fused to such a promoter has to rely on its original genetic signal for controlling the synthesis of its protein product.

Detailed Description Text (43):

Construction of plasmid pLNH21 (also designated as pLSK15-KD-AR) and transformation of *S. cerevisiae* and 1400 with pLNH21

Detailed Description Text (44):

The construction of pLNH21 is outlined in FIG. 12. pLNH21 was used to transform *S. cerevisiae* and strain 1400 by electroporation under the following conditions. Fifty ml yeast cells, grown to early log phase (Klett Unit (KU) 130), were centrifuged to remove the medium, washed twice with cold water, once with cold 1M sorbitol, and resuspended in 200 .mu.l 1M sorbitol. Sixty .mu.l of the cells were transferred into a 4 ml presterilized plastic tube (with cap) and to which 0.1 .mu.g to 1 .mu.g plasmid DNA was added. Fifty .mu.l of the resulting cells and plasmid mixture were pipetted into a precooled gene pulser cuvette with a 0.2 cm electrode gap and the content in the cuvette was subjected to pulse by the gene pulser with a pulse controller (BioRad) at 2.0 KV, 25 .mu.F, 200 ohms.

Detailed Description Text (46):

Transformation of strain 1400 with pLNH21 or other plasmids was carried out using a similar procedure to that described above, except that the cells were grown to 140-190 KU rather than 130 KU and the YEPD plates for the initial selection of

transformants after electroporation contained 40 .mu.g/ml geneticin G418 rather than 50. Transformation of strain 1400 by the above described procedures was not as effective as transformation of *S. cerevisiae*.

Detailed Description Text (49):

These three yeasts were cultured in rich medium YEPD aerobically under identical conditions (SC(pLNH13-32) was constructed by transforming *S. cerevisiae* with a plasmid, designated pLNH13-32, which contains only the XR and XD gene/promotor combinations). These yeast cells were then used to ferment 5% xylose in YEP (1% yeast extract, 2% peptone) medium anaerobically also under identical conditions. The consumption of xylose and the formation of ethanol and xylitol were followed during fermentation by taking samples at proper intervals and analyzing them by HPLC under the following conditions.

Detailed Description Text (61):

When the cell density reached mid-log phase (400 Klett units), 12.5 ml (40%) glucose and 6.25 ml (40%) xylose were added to each flask. After thorough mixing, 1 ml of the culture mixture was removed from the flask to serve as the zero sample. The flask was then sealed with Saran wrap to allow fermentation to be carried out anaerobically. One ml samples of the fermentation broth (with some cells) were removed at proper intervals (every 24 hr.) to serve as samples for measuring the sugar and ethanol contents of the broth during fermentation. The ethanol, glucose, xylose, and xylitol contents of the samples were analyzed by HPLC as described in Example 6. The results, shown in FIGS. 8A and 8B, demonstrate that the genetically engineered yeast 1400(pLNH33) can ferment 10% glucose and 5% xylose to ethanol simultaneously in two to four days without requiring high cell density. On the other hand, the parent strain 1400 can only convert glucose to ethanol but not xylose. The fermentation was carried out under normal conditions, without requiring special medium, special pH, and also without requiring growth of yeast to high cell density. Thus the genetically engineered 1400(pLNH33) containing the XR, XD, and XK, all fused to glycolytic promoters and cloned on a high copy-number plasmid pUCKm10, can ferment high concentrations of both glucose and xylose simultaneously to ethanol in two to four days with very little xylitol produced as a by-product.

Detailed Description Text (78):

Chevallier, M. R. and M. Aigle, "Qualitative detection of penicillinase produced by yeast strains carrying chimeric yeast-coli plasmids," FEBS Letters, 108(1) 179-184 (1979).

Other Reference Publication (6):

Chevallier, M. R. and M. Aigle, "Qualitative detection of penicillinase produced by yeast strains carrying chimeric yeast-coli plasmids," FEBS Letters, 108(1) 179-184 (1979).

=&gt; d his

(FILE 'HOME' ENTERED AT 15:35:08 ON 04 MAR 2004)

FILE 'REGISTRY' ENTERED AT 15:35:42 ON 04 MAR 2004

```

SET COST OFF
E XYLOSE REDUCTASE/CN
L1      4 S E3
E XYLITOL DEHYDROGENASE/CN
L2      2 S E3
E XYLULOKINASE/CN
L3      1 S E3
L4      26 S XYLOSE REDUCTASE
L5      7 S XYLITOL DEHYDROGENASE
L6      33 S XYLULOKINASE

```

FILE 'HCAPLUS' ENTERED AT 15:37:10 ON 04 MAR 2004

```

L7      2967 S L1-L6
L8      464 S XYLOSE REDUCTASE OR XYLITOL DEHYDROGENASE OR XYLULOKINASE
L9      3153 S ALDOSE REDUCTASE
L10     68 S XYLULOSE REDUCTASE
L11     50 S XYLULOSE KINASE
L12     3760 S L7-L11
L13     218 S L12 AND YEAST
E YEAST/CT
L14     25 S L12 AND E3-E53
E E53+ALL
L15     12225 S E1
E E2+ALL
L16     34588 S E6,E5+NT
L17     25 S L12 AND L15,L16
L18     218 S L13,L14,L17
L19     1 S YEAST(L) 1400 (L) LNH(L) ST
E SACCHAROMYCES/CT
L20     9 S L12 AND E3
L21     114 S L12 AND E3-E196
E E3+ALL
L22     0 S L12 AND E4
L23     113 S L12 AND E5+NT
L24     269 S L18,L20-L23
L25     32 S L24 AND DNA
L26     31 S L24 AND PLASMID
L27     20 S L24 AND CHROMOSOM?
L28     126 S L24 AND GENE
L29     74 S L24 AND GENETIC?/SC,SX
L30     130 S L25-L29
L31     269 S L24-L30
E WO97-US7663/AP,PRN
L32     1 S E3,E4
E US96-016865/AP,PRN
L33     1 S E5
E HO N/AU
L34     20 S E3,E11,E12
L35     36 S E28,E31,E32
E CHEN Z/AU
L36     722 S E3,E7
E CHEN ZHENG/AU
L37     261 S E3,E4
L38     8 S E51
L39     1 S L31 AND L32,L33
L40     11 S L31 AND L34-L38
L41     11 S L32,L33,L39,L40
L42     134 S L31 AND (PD<=19960506 OR PRD<=19960506 OR AD<=19960506)

```

L43 9 S L41 AND L42  
L44 11 S L41,L43  
L45 27 S L42 AND GENETIC?/SC,SX  
L46 31 S L44,L45  
L47 105 S L42 NOT L46  
SEL DN AN 22 34 L47  
L48 2 S E1-E6 AND L47  
L49 33 S L46,L48 AND L7-L48  
SEL HIT RN

FILE 'REGISTRY' ENTERED AT 16:16:43 ON 04 MAR 2004

L50 14 S E7-E20  
L51 14 S L50 AND L1-L6

=> fil reg

FILE 'REGISTRY' ENTERED AT 16:17:14 ON 04 MAR 2004  
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provided by InfoChem.

STRUCTURE FILE UPDATES: 3 MAR 2004 HIGHEST RN 658036-92-1  
DICTIONARY FILE UPDATES: 3 MAR 2004 HIGHEST RN 658036-92-1

TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2003

Please note that search-term pricing does apply when  
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more  
information enter HELP PROP at an arrow prompt in the file or refer  
to the file summary sheet on the web at:  
<http://www.cas.org/ONLINE/DBSS/registryss.html>

=> d ide can tot l51

L51 ANSWER 1 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 183399-64-6 REGISTRY  
CN DNA (Pachysolen tannophilus clone pBS1554 aldose reductase gene plus  
flanks) (9CI) (CA INDEX NAME)  
OTHER CA INDEX NAMES:  
CN Deoxyribonucleic acid (Pachysolen tannophilus clone pBS1554 aldose  
reductase gene plus 5'- and 3'-flanking region fragment)  
OTHER NAMES:  
CN Deoxyribonucleic acid (Pachysolen tannophilus clone pBS1554 aldose  
(xylose) reductase gene plus 5'- and 3'-flanking region fragment)  
CN GenBank U40706  
FS NUCLEIC ACID SEQUENCE  
MF Unspecified  
CI MAN  
SR GenBank  
LC STN Files: BIOSIS, CA, CAPLUS, GENBANK

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
\*\*\* USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE \*\*\*  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 126:2045

L51 ANSWER 2 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 183327-22-2 REGISTRY  
CN Reductase, aldose (Pachysolen tannophilus clone pBS1554 reduced) (9CI)  
(CA INDEX NAME)

## OTHER NAMES:

CN Aldose (xylose) reductase (Pachysolen tannophilus clone pBS1554 reduced) (E.C. 1.1.1.21)  
CN GenBank AAC49526  
CN GenBank AAC49526 (Translated from: GenBank U40706)  
FS PROTEIN SEQUENCE  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

\*\*\* USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE \*\*\*  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 126:2045

L51 ANSWER 3 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 167974-35-8 REGISTRY  
CN DNA (Saccharomyces cerevisiae strain 1400 clone pLNH33 xylulokinase gene plus flanks) (9CI) (CA INDEX NAME)

## OTHER CA INDEX NAMES:

CN Deoxyribonucleic acid (Saccharomyces cerevisiae strain 1400 clone pLNH33 xylulokinase gene plus 5'- and 3'-flanking region fragment)  
FS NUCLEIC ACID SEQUENCE  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, USPATFULL

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
\*\*\* USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE \*\*\*  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 123:196764

L51 ANSWER 4 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 167078-89-9 REGISTRY  
CN Xylulokinase (Saccharomyces cerevisiae strain 1400 clone pLNH33 reduced) (9CI) (CA INDEX NAME)

FS PROTEIN SEQUENCE  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, USPATFULL

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
\*\*\* USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE \*\*\*  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 123:196764

L51 ANSWER 5 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 146409-22-5 REGISTRY  
CN DNA (Yamadazyma stipitis clone pUA103 gene XYL1) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN Deoxyribonucleic acid (Pichia stipitis xylose reductase gene XYL1)  
FS NUCLEIC ACID SEQUENCE  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
\*\*\* USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE \*\*\*  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 118:123016

L51 ANSWER 6 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 146409-21-4 REGISTRY  
CN DNA (Yamadazyma stipitis clone pUA103 gene XYL1 plus flanks) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN Deoxyribonucleic acid (Pichia stipitis xylose reductase gene XYL1 plus 5'- and 3'-flanking region fragment)  
FS NUCLEIC ACID SEQUENCE  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
\*\*\* USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE \*\*\*  
1 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 118:123016

L51 ANSWER 7 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 138263-97-5 REGISTRY  
CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide (phosphate)) (Yamadazyma stipitis clone pUA103 gene XYL1 precursor reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:  
CN NADH/NADPH-dependent xylose reductase (Pichia stipitis reduced)  
CN Xylose reductase (Pichia stipitis reduced)  
FS PROTEIN SEQUENCE  
MF Unspecified  
CI MAN  
SR CA  
LC STN Files: CA, CAPLUS, USPATFULL

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
\*\*\* USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE \*\*\*  
5 REFERENCES IN FILE CA (1907 TO DATE)  
5 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 118:226769

REFERENCE 2: 118:123016

REFERENCE 3: 118:96990

REFERENCE 4: 116:52957

REFERENCE 5: 116:35663

L51 ANSWER 8 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN

RN 121548-71-8 REGISTRY

CN Protein (Saccharomyces cerevisiae gene GCY reduced) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 40: PN: W00155342 SEQID: 42 claimed protein

CN Protein (Saccharomyces cerevisiae clone pEOA306/pEOA265/pEOA106 gene GCY)

CN Protein (Saccharomyces cerevisiae clone pEOA347 gene GCY)

CN Protein (Saccharomyces cerevisiae gene GCY1)

CN Reductase, aldose (Saccharomyces cerevisiae gene AKR-A)

CN **Xylose reductase (Saccharomyces cerevisiae open reading frame YJR096W)**

FS PROTEIN SEQUENCE

MF Unspecified

CI MAN

SR CA

LC STN Files: CA, CAPLUS, USPATFULL

**\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\***

**\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\***

**\*\*\* USE 'SQD' OR 'SQIDE' FORMATS TO DISPLAY SEQUENCE \*\*\***

6 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

6 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 136:2117

REFERENCE 2: 135:148225

REFERENCE 3: 127:219657

REFERENCE 4: 127:131709

REFERENCE 5: 124:252209

REFERENCE 6: 111:34409

L51 ANSWER 9 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN

RN 104118-53-8 REGISTRY

CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide phosphate) (9CI) (CA INDEX NAME)

OTHER NAMES:

CN **D-Xylose reductase**

CN **D-Xylose reductase (NADPH)**

CN **NADPH-dependent xylose reductase**

CN Reductase, xylose (reduced nicotinamide adenine dinucleotide phosphate)

CN **Xylose reductase**

DR 163913-54-0

MF Unspecified

CI MAN

SR CA

LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CIN, PIRA, TOXCENTER

**\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\***

29 REFERENCES IN FILE CA (1907 TO DATE)

## 29 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:107416  
REFERENCE 2: 140:14605  
REFERENCE 3: 138:400479  
REFERENCE 4: 138:86217  
REFERENCE 5: 137:335006  
REFERENCE 6: 135:223422  
REFERENCE 7: 135:136473  
REFERENCE 8: 133:360695  
REFERENCE 9: 132:11668  
REFERENCE 10: 131:227744

L51 ANSWER 10 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN

RN 99775-25-4 REGISTRY

CN Reductase, D-xylose (9CI) (CA INDEX NAME)

OTHER NAMES:

CN D-Xylose reductase

CN NADH-dependent xylose reductase

CN Xylose reductase

MF Unspecified

CI MAN

SR CA

LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CIN, PIRA,  
TOXCENTER, USPATFULL

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

51 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

51 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 139:225259  
REFERENCE 2: 139:178733  
REFERENCE 3: 139:65901  
REFERENCE 4: 138:283215  
REFERENCE 5: 138:166431  
REFERENCE 6: 138:54597  
REFERENCE 7: 138:54591  
REFERENCE 8: 137:139426  
REFERENCE 9: 137:30383  
REFERENCE 10: 136:147534

L51 ANSWER 11 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN

RN 95829-40-6 REGISTRY

CN Reductase, D-xylose (reduced nicotinamide adenine dinucleotide



(phosphate)) (9CI) (CA INDEX NAME)  
OTHER NAMES:

CN **D-Xylose reductase**  
CN NAD(P)H-dependent aldose reductase  
CN **NAD(P)H-dependent xylose reductase**  
CN **NADPH-D-xylose reductase**  
CN **Xylose reductase**  
MF Unspecified  
CI MAN  
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CIN, PIRA, PROMT,  
TOXCENTER, USPATFULL

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
79 REFERENCES IN FILE CA (1907 TO DATE)  
2 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA  
79 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:107416  
REFERENCE 2: 140:55544  
REFERENCE 3: 140:14605  
REFERENCE 4: 139:394971  
REFERENCE 5: 139:394931  
REFERENCE 6: 139:360858  
REFERENCE 7: 139:260078  
REFERENCE 8: 139:260077  
REFERENCE 9: 139:226255  
REFERENCE 10: 139:176481

L51 ANSWER 12 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN  
RN **9030-58-4** REGISTRY  
CN Kinase (phosphorylating), xylulo- (9CI) (CA INDEX NAME)  
OTHER NAMES:

CN **D-Xylulokinase**  
CN D-Xylulose kinase  
CN E.C. 2.7.1.17  
CN **Xylulokinase**  
CN Xylulose kinase  
DR 57127-28-3  
MF Unspecified  
CI MAN  
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS, CIN,  
EMBASE, PIRA, TOXCENTER, USPATFULL

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*  
154 REFERENCES IN FILE CA (1907 TO DATE)  
1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA  
154 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:144753  
REFERENCE 2: 140:127260  
REFERENCE 3: 140:107886

REFERENCE 4: 139:347843  
REFERENCE 5: 139:260078  
REFERENCE 6: 139:260077  
REFERENCE 7: 139:226997  
REFERENCE 8: 139:225259  
REFERENCE 9: 139:178733  
REFERENCE 10: 139:163668

L51 ANSWER 13 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN

RN 9028-31-3 REGISTRY

CN Reductase, aldose (9CI) (CA INDEX NAME)

OTHER NAMES:

CN Aldose reductase

CN D-Ribose reductase

CN E.C. 1.1.1.21

CN L-Arabinose reductase

CN NADPH-aldopentose reductase

CN NADPH-aldose reductase

CN NADPH-dependent aldose reductase

CN NADPH-L-arabinose reductase

CN **Xylose reductase**

MF Unspecified

CI MAN

LC STN Files: ADISNEWS, AGRICOLA, ANABSTR, BIOBUSINESS, BIOSIS, BIOTECHNO,  
CA, CAPLUS, CASREACT, CEN, CIN, EMBASE, IFICDB, IFIPAT, IFIUDB,  
NAPRALERT, PIRA, PROMT, TOXCENTER, USPAT2, USPATFULL

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

2523 REFERENCES IN FILE CA (1907 TO DATE)

20 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

2531 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:146002  
REFERENCE 2: 140:127260  
REFERENCE 3: 140:111411  
REFERENCE 4: 140:108742  
REFERENCE 5: 140:108579  
REFERENCE 6: 140:106718  
REFERENCE 7: 140:104477  
REFERENCE 8: 140:104459  
REFERENCE 9: 140:104246  
REFERENCE 10: 140:94037

L51 ANSWER 14 OF 14 REGISTRY COPYRIGHT 2004 ACS on STN

RN 9028-16-4 REGISTRY

CN Reductase, D-xylose (9CI) (CA INDEX NAME)

OTHER NAMES:

CN 2,3-cis-Polyol dehydrogenase

CN D-Xylulose reductase  
CN Dehydrogenase, 2,3-cis-polyol  
CN E.C. 1.1.1.9  
CN Erythritol dehydrogenase  
CN NAD-dependent meso-erythritol dehydrogenase  
CN **NAD-dependent xylitol dehydrogenase**  
CN Polyol dehydrogenase  
CN **Xylitol dehydrogenase**  
DR 9032-74-0  
MF Unspecified  
CI MAN  
LC STN Files: AGRICOLA, BIOBUSINESS, BIOSIS, BIOTECHNO, CA, CAPLUS,  
CASREACT, CIN, EMBASE, PIRA, TOXCENTER, USPATFULL

\*\*\* STRUCTURE DIAGRAM IS NOT AVAILABLE \*\*\*

213 REFERENCES IN FILE CA (1907 TO DATE)

1 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA

214 REFERENCES IN FILE CAPLUS (1907 TO DATE)

REFERENCE 1: 140:127260  
REFERENCE 2: 140:24162  
REFERENCE 3: 140:14605  
REFERENCE 4: 139:260078  
REFERENCE 5: 139:260077  
REFERENCE 6: 139:226997  
REFERENCE 7: 139:225259  
REFERENCE 8: 139:178733  
REFERENCE 9: 139:176481  
REFERENCE 10: 139:163668

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 16:17:29 ON 04 MAR 2004

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FILE COVERS 1907 - 4 Mar 2004 VOL 140 ISS 10  
FILE LAST UPDATED: 3 Mar 2004 (20040303/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

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L49 ANSWER 1 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 2003:486085 HCAPLUS  
 DN 139:225259  
 ED Entered STN: 26 Jun 2003  
 TI **DNA** microarray analysis of the expression of the **genes**  
 encoding the major enzymes in ethanol production during glucose and xylose  
 co-fermentation by metabolically engineered **Saccharomyces yeast**  
 AU Sedlak, Miroslav; Edenberg, Howard J.; Ho, Nancy W. Y.  
 CS School of Engineering, Laboratory of Renewable Resources Engineering,  
 Purdue University, West Lafayette, IN, 47907-2022, USA  
 SO Enzyme and Microbial Technology (2003), 33(1), 19-28  
 CODEN: EMTED2; ISSN: 0141-0229  
 PB Elsevier Science  
 DT Journal  
 LA English  
 CC 3-3 (Biochemical Genetics)  
 Section cross-reference(s): 10, 16  
 AB Lignocellulosic biomass, which contains large amts. of glucose and xylose,  
 is the new ideal feedstock for ethanol production used as renewable liquid fuel  
 for transportation. The naturally occurring **Saccharomyces yeasts**  
 traditionally used for industrial ethanol production are unable to ferment  
 xylose. The authors have successfully developed genetically engineered  
**Saccharomyces yeasts** that can effectively co-ferment both  
 glucose and xylose simultaneously to ethanol. The engineered  
**yeast** contains three xylose metabolizing **genes**, the  
**xylose reductase (XR)**, **xylitol**  
**dehydrogenase (XD)** and **xylulokinase (XK) genes**  
 , fused to glycolytic promoters, on high copy **plasmids** or  
 integrated into the **yeast chromosome** in multiple  
 copies. Although the glucose/xylose co-fermenting **yeasts** are  
 currently the most effective **yeast** for producing ethanol from  
 cellulosic biomass, they still utilize glucose more efficiently than  
 xylose. The authors believe that carefully analyzing **gene**  
 expression during co-fermentation of glucose and xylose to ethanol, using the  
 genetically modified strains, will reveal ways to optimize xylose fermentation  
 In this paper, the authors report the results on analyzing the expression  
 of **genes** in the glycolytic and alc. fermentation pathways using  
 microarray technol. The authors also report the results on the anal. of  
 the activities of the selected enzymes for ethanol production during  
 co-fermentation  
 of glucose and xylose to ethanol by one of the effective glucose/xylose  
 co-fermenting **yeasts** 424A(LNH-ST).  
 ST **DNA** microarray ethanol glucose xylose fermn **Saccharomyces**  
 IT **Saccharomyces cerevisiae**  
 (424A(LNH-ST); **DNA** microarray anal. of **genes**  
 encoding enzymes involved in glycolysis and alc. fermentation glucose and  
 xylose co-fermentation by metabolically engineered **Saccharomyces**  
**yeast** 424A(LNH-ST))  
 IT **Gene**, microbial  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (ADH1; **DNA** microarray anal. of **genes** encoding  
 enzymes involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by metabolically engineered **Saccharomyces yeast**  
 424A(LNH-ST))  
 IT **Gene**, microbial  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (ADH2; **DNA** microarray anal. of **genes** encoding  
 enzymes involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by metabolically engineered **Saccharomyces yeast**  
 424A(LNH-ST))

hand date

- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(ADH3; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(ADH4; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT **DNA microarray technology**  
(Affymetrix; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT Fermentation  
**Gene expression profiles, microbial**  
Genetic engineering  
Glycolysis  
(**DNA** microarray anal. of **genes** encoding enzymes  
involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by  
metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(ENO1; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(ENO2; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(FBI1; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(GLK1; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(GPM1; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(H XK1; **DNA** microarray anal. of **genes** encoding  
enzymes involved in glycolysis and alc. fermentation glucose and xylose  
co-fermentation by metabolically engineered *Saccharomyces yeast*  
424A(LNH-ST))
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)

- (HXK2; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PDC1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PDC5; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PDC6; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PFK1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PFK2; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PGI1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PGK1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PYK1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(PYK2; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(TDH1; **DNA** microarray anal. of **genes** encoding enzymes involved in glycolysis and alc. fermentation glucose and xylose co-fermentation by metabolically engineered *Saccharomyces yeast*

- 424A(LNH-ST))
- IT **Gene**, microbial  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (TDH2; **DNA** microarray anal. of **genes** encoding  
 enzymes involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by metabolically engineered *Saccharomyces yeast*  
 424A(LNH-ST))
- IT **Gene**, microbial  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (TDH3; **DNA** microarray anal. of **genes** encoding  
 enzymes involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by metabolically engineered *Saccharomyces yeast*  
 424A(LNH-ST))
- IT **Gene**, microbial  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (TPI1; **DNA** microarray anal. of **genes** encoding  
 enzymes involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by metabolically engineered *Saccharomyces yeast*  
 424A(LNH-ST))
- IT Enzymes, biological studies  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (glycolytic; **DNA** microarray anal. of **genes** encoding  
 enzymes involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by metabolically engineered *Saccharomyces yeast*  
 424A(LNH-ST))
- IT 64-17-5, Ethanol, biological studies 591-59-3 9001-04-1, Pyruvate  
 decarboxylase 9001-59-6, Pyruvate kinase 9001-83-6, Phosphoglycerate  
 kinase 9031-72-5, Alcohol dehydrogenase  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (**DNA** microarray anal. of **genes** encoding enzymes  
 involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by  
 metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT 50-99-7, D-Glucose, biological studies 58-86-6, Xylose, biological  
 studies  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES  
 (Uses)  
 (**DNA** microarray anal. of **genes** encoding enzymes  
 involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by  
 metabolically engineered *Saccharomyces yeast* 424A(LNH-ST))
- IT 9028-16-4, Xylitol dehydrogenase  
 9030-58-4, Xylulokinase 99775-25-4,  
**Xylose reductase**  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES  
 (Uses)  
 (**DNA** microarray anal. of **genes** encoding enzymes  
 involved in glycolysis and alc. fermentation glucose and xylose  
 co-fermentation by  
 metabolically engineered *Saccharomyces yeast* 424A(LNH-ST)  
 containing)

RE.CNT 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD  
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 (11) Walfridsson, M; Appl Microbiol Biotechnol 1997, V48, P218 HCAPLUS

L49 ANSWER 2 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 2003:282043 HCAPLUS  
 DN 138:302748  
 ED Entered STN: 11 Apr 2003  
 TI Manufacture of five-carbon sugars and sugar alcohols  
 IN Miasnikov, Andrei; Ojamo, Heikki; Povelainen, Mira; Gros, Hakan; Toivari, Mervi; Richard, Peter; Ruohonen, Laura; Koivuranta, Kari; Londesborough, John; Aristidou, Aristos; Penttila, Merja; Plazanet-Menut, Claire; Deutscher, Josef  
 PA Xyrofin Oy, Finland  
 SO U.S. Pat. Appl. Publ., 96 pp., Cont.-in-part of U.S. Ser. No. 488,581, abandoned.  
 CODEN: USXXCO  
 DT Patent  
 LA English  
 IC ICM C12P007-18  
 ICS C12N001-21; C12N001-18  
 NCL 435158000; 435252300; 435254200  
 CC 16-2 (Fermentation and Bioindustrial Chemistry)  
 Section cross-reference(s): 3  
 FAN.CNT 3

|    | PATENT NO.    | KIND   | DATE     | APPLICATION NO. | DATE         |
|----|---------------|--|----------|-----------------|--------------|
| PI | US 2003068791 | A1   | 20030410 | US 2001-908744  | 20010720 <-- |
|    | HU 72187      | A2   | 19960328 | HU 1995-1288    | 19931105 <-- |
|    | HU 219016     | B  | 20010129 |                 |              |
|    | AT 184917     | E  | 19991015 | AT 1993-924615  | 19931105 <-- |
|    | ES 2139024    | T3   | 20000201 | ES 1993-924615  | 19931105 <-- |
|    | US 5631150    | A  | 19970520 | US 1995-368395  | 19950103 <-- |
|    | WO 2001053306 | A2   | 20010726 | WO 2001-FI51    | 20010122     |
|    | WO 2001053306 | A3   | 20020418 |                 |              |
|    | W:            | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM |          |                 |              |
|    | RW:           | GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG   |          |                 |              |

PRAI US 1992-973325 B2 19921105 <--  
 US 1993-110672 B1 19930824 <--  
 US 1995-368395 A1 19950103 <--  
 US 1997-790585 A2 19970129  
 US 2000-488581 B2 20000121  
 WO 2001-FI51 A2 20010122

AB The invention relates to the methods of manufacturing C5 sugars and sugar alcs. as well as other compds. derived from the pentose phosphate pathway from readily available substrates such as hexoses using metabolically engineered microbial hosts.

ST pentose pentitol fermn bacteria genetic engineering; **gene**  
 sequence xylitol arabitol phosphate dehydrogenase

IT **Gene**, microbial

RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (APDH; manufacture of five-carbon sugars and sugar alcs.)

IT **Gene**, microbial

RL: BSU (Biological study, unclassified); BIOL (Biological study)  
 (DOG1; manufacture of five-carbon sugars and sugar alcs.)

IT **Gene**, microbial



RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(LTP1; manufacture of five-carbon sugars and sugar alcs.)

IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(XPDH; manufacture of five-carbon sugars and sugar alcs.)

IT **DNA sequences**  
Protein sequences  
(bacterial xylitol and arabitol phosphphate dehydrogenases)

IT **Bacillus subtilis**  
Genetic engineering  
Pentose phosphate pathway  
**Saccharomyces cerevisiae**  
(manufacture of five-carbon sugars and sugar alcs.)

IT **Alditols**  
Pentoses  
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL  
(Biological study); PREP (Preparation)  
(manufacture of five-carbon sugars and sugar alcs.)

IT **Bacillus halodurans**  
Enterococcus avium  
Lactobacillus rhamnosus  
(manufacture of five-carbon sugars and sugar alcs. with enzyme from)

IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(rpi; manufacture of five-carbon sugars and sugar alcs.)

IT 510787-74-3 510787-76-5  
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(amino acid sequence; manufacture of five-carbon sugars and sugar alcs.)

IT 9035-82-9, Dehydrogenase  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(for arabitol phosphate; manufacture of five-carbon sugars and sugar alcs.)

IT 87-99-0P, Xylitol 488-81-3P, Ribitol 488-82-4P, D-Arabitol  
488-84-6P, D-Ribulose 551-84-8P, D-Xylulose 1114-34-7P, D-Lyxose  
6917-36-8P, Pentitol 10323-20-3P, D-Arabinose  
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL  
(Biological study); PREP (Preparation)  
(manufacture of five-carbon sugars and sugar alcs.)

IT **9028-16-4, Xylitol dehydrogenase** 64886-68-6,  
Xylitol phosphate dehydrogenase  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(manufacture of five-carbon sugars and sugar alcs.)

IT 510787-75-4 510787-77-6  
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL  
(Biological study)  
(nucleotide sequence; manufacture of five-carbon sugars and sugar alcs.)

IT 510944-98-6 510944-99-7 510945-00-3 510945-01-4 510945-02-5  
510945-03-6 510945-04-7 510945-05-8 510945-06-9 510945-07-0  
510945-08-1 510945-09-2 510945-10-5 510945-11-6 510945-12-7  
510945-13-8 510945-14-9 510945-15-0 510945-16-1 510945-17-2  
510945-18-3 510945-19-4 510945-20-7 510945-21-8 510945-23-0  
510945-25-2 510945-26-3 510945-31-0 510945-32-1 510945-33-2  
510945-34-3 510945-35-4 510945-36-5 510945-37-6 510945-38-7  
510945-39-8 510945-40-1 510945-42-3 510945-43-4 510945-44-5  
510945-45-6 510945-46-7 510945-47-8 510945-48-9 510945-49-0  
510945-50-3 510945-51-4 510945-52-5 510945-53-6 510945-54-7  
510945-55-8  
RL: PRP (Properties)  
(unclaimed nucleotide sequence; manufacture of five-carbon sugars and sugar  
alcs.)

IT 510945-22-9 510945-24-1 510945-27-4 510945-28-5 510945-29-6  
510945-30-9 510945-41-2  
RL: PRP (Properties)

(unclaimed protein sequence; manufacture of five-carbon sugars and sugar alcs.)

IT 351900-48-6 351900-49-7 351900-50-0 351900-51-1 351900-52-2  
351900-53-3 351900-54-4 351900-55-5

RL: PRP (Properties)

(unclaimed sequence; manufacture of five-carbon sugars and sugar alcs.)

L49 ANSWER 3 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 2001:545704 HCAPLUS

DN 135:136473

ED Entered STN: 27 Jul 2001

TI Manufacture of five-carbon sugars and sugar alcohols using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway

IN Miasnikov, Andrei; Ojamo, Heikki; Povelainen, Mira; Gros, Hakan; Toivari, Mervi; Richard, Peter; Ruohonen, Laura; Koivuranta, Kari; Londesborough, John; Aristidou, Aristos; Penttilae, Merja; Plazanet-Menut, Claire; Deutscher, Josef

PA Xyrofin Oy, Finland

SO PCT Int. Appl., 205 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C07H

CC 16-2 (Fermentation and Bioindustrial Chemistry)

Section cross-reference(s): 3, 6, 10, 33

FAN.CNT 3

|      | PATENT NO.   | KIND | DATE     | APPLICATION NO. | DATE         |
|------|--|------|----------|-----------------|--------------|
| PI   | WO 2001053306  | A2   | 20010726 | WO 2001-FI51    | 20010122     |
|      | WO 2001053306  | A3   | 20020418 |                 |              |
|      | W:   |      |          |                 |              |
|      | AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM |      |          |                 |              |
|      | RW:  |      |          |                 |              |
|      | GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG   |      |          |                 |              |
|      | AU 2001031784  | A5   | 20010731 | AU 2001-31784   | 20010122     |
|      | BR 2001007918  | A    | 20021105 | BR 2001-7918    | 20010122     |
|      | EP 1254244   | A2   | 20021106 | EP 2001-903815  | 20010122     |
|      | R:   |      |          |                 |              |
|      | AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR   |      |          |                 |              |
|      | JP 2003520583  | T2   | 20030708 | JP 2001-553780  | 20010122     |
|      | US 2003068791  | A1   | 20030410 | US 2001-908744  | 20010720 <-- |
| PRAI | US 2000-488581   | A    | 20000121 |                 |              |
|      | US 1992-973325   | B2   | 19921105 | <--             |              |
|      | US 1993-110672   | B1   | 19930824 | <--             |              |
|      | US 1995-368395   | A1   | 19950103 | <--             |              |
|      | US 1997-790585   | A2   | 19970129 |                 |              |
|      | WO 2001-FI51   | W    | 20010122 |                 |              |

AB The invention relates to the methods of manufacturing five-carbon sugars and sugar alcs. as well as other compds. derived from pentose-phosphate pathway (PPP) from readily available substrates such a hexoses using metabolically engineered microbial hosts. A series of the **genes** involved in the PPP are cloned from various microorganisms or disrupted in the host of either Bacillus subtilis or Saccharomyces cerevisiae. This strategy is demonstrated to successfully increase the yield of a variety of the five-carbon sugar or sugar alcs. for manufacturing purpose.

ST five carbon sugar alc fermn Bacillus Saccharomyces PPP **gene**;

pentose phosphate pathway **gene** mutagenesis overexpression  
transformation fermn

- IT **Plasmid vectors**  
(B1003, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(B1011, **gene** IDP2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(B1068, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(B11154, **gene** XKS1 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(B1187, **gene** PGI1 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(B1449, **gene** LTP1 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(B995, **gene** XYL2 on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Klebsiella terrigena**  
(D-xylulose-forming arabitol dehydrogenase **gene**; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(DOG1, for 2-deoxyglucose-6-phosphate phosphatase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(DOG2, for 2-deoxyglucose-6-phosphate phosphatase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(GDH2, expression in Pichia stipitis of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(LTP, for Low Mol. Weight Protein-Tyrosine Phosphatase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(LTP1, for Low Mol. Weight Protein-Tyrosine Phosphatase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or

- transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); PROC (Process); USES (Uses)  
(MAE1, overexpression and carbon source utilization in *Saccharomyces cerevisiae*; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT *Peptoniphilus asaccharolyticus*  
(NAD-glutamate dehydrogenase of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(PFK26, for 6-phosphofructo-L-kinase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(PFK27, for 6-phosphofructo-L-kinase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(PGI1, for phosphoglucoisomerase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
(PPPasel; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
(PPPasel2; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(TKL1; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(TKL2; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT *Morganella morganii*  
(XDH (**xylitol dehydrogenase**) **gene** cloned from; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)

- (XK, expression in *Pichia stipitis* of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
 RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
 (XYL1, for **xylose reductase**; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
 RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
 (XYL2, for xylose dehydrogenase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT Fermentation  
 (anaerobic; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT Hexoses  
 Pentoses  
 Polysaccharides, biological studies  
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
 (as carbon source; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT Redox reaction  
 (biochem., electron transport using; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT Brevibacterium  
 Corynebacterium  
 (fermentation host; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT *Pichia*  
**Saccharomyces**  
*Schizosaccharomyces*  
*Schizosaccharomyces pombe*  
*Yamadazyma*  
*Yamadazyma stipitis*  
 (fermentation using; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT Michaelis constant  
 (for nicotinamide coenzymes of malic enzyme of **yeast**; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene, microbial**  
 RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
 (fucI, for L-fucose isomerase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT *Ralstonia eutropha*  
 (**genes** for polyhydroxybutyrate biosynthetic enzymes of, expression in **yeast** of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT Operon  
 (glcUgdh; manufacture of five-carbon sugars and sugar alcs. using

- microorganisms deficient in or transformed with **genes**  
involved in pentose-phosphate pathway)
- IT Biological transport  
(glucose; manufacture of five-carbon sugars and sugar alcs. using  
microorganisms deficient in or transformed with **genes**  
involved in pentose-phosphate pathway)
- IT Carboxylic acids, preparation  
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP  
(Preparation)  
(hydroxy, polymers, fermentation of; manufacture of five-carbon sugars and  
sugar  
alcs. using microorganisms deficient in or transformed with  
**genes** involved in pentose-phosphate pathway)
- IT *Pseudomonas cichorii*  
(ketose 3-epimerase **gene** of; manufacture of five-carbon sugars and  
sugar alcs. using microorganisms deficient in or transformed with  
**genes** involved in pentose-phosphate pathway)
- IT *Corynebacterium glutamicum*  
(lysine fermentation with transgenic; manufacture of five-carbon sugars and  
sugar  
alcs. using microorganisms deficient in or transformed with  
**genes** involved in pentose-phosphate pathway)
- IT *Aspergillus nidulans*  
(malic enzyme of, expression in *Pichia* of **gene** for; manufacture of  
five-carbon sugars and sugar alcs. using microorganisms deficient in or  
transformed with **genes** involved in pentose-phosphate pathway)
- IT *Bacillus halodurans*  
*Bacillus subtilis*  
Biomass  
*Clostridium difficile*  
DNA sequences  
Electron transport system, biological  
*Enterococcus avium*  
Fermentation  
*Lactobacillus rhamnosus*  
Molecular cloning  
Mutagenesis  
Pentose phosphate pathway  
Protein sequences  
*Trichoderma reesei*  
*Zygosaccharomyces rouxii*  
(manufacture of five-carbon sugars and sugar alcs. using microorganisms  
deficient in or transformed with **genes** involved in  
pentose-phosphate pathway)
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BUU (Biological use,  
unclassified); BIOL (Biological study); USES (Uses)  
(manufacture of five-carbon sugars and sugar alcs. using microorganisms  
deficient in or transformed with **genes** involved in  
pentose-phosphate pathway)
- IT Promoter (genetic element)  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES  
(Uses)  
(manufacture of five-carbon sugars and sugar alcs. using microorganisms  
deficient in or transformed with **genes** involved in  
pentose-phosphate pathway)
- IT Coenzymes  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL  
(Biological study); PROC (Process)  
(nicotinamide; manufacture of five-carbon sugars and sugar alcs. using  
microorganisms deficient in or transformed with **genes**  
involved in pentose-phosphate pathway)
- IT Enzyme kinetics

(of malic enzyme of *Saccharomyces cerevisiae*; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

- IT **Plasmid vectors**  
(p131, **rpi gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(p131:Cm-2, **rpi gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pAOS63, **gene XYL2** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pAOS64, **gene XYL2** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pAOS66, **XYL1** and **XYL2 genes** on, expression in *Pichia stipitis* of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pAOS67, **gene XYL2** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pBS(AR2T), D-ribulose-5-phosphate epimerase **gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pBS(AR2T)-kan, D-ribulose-5-phosphate epimerase **gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pBS, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pGT21, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pGT23, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pGTK24(MXD2), **xylitol dehydrogenase gene** on; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pGTK24, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Plasmid vectors**  
(pTKT:E1, cloning vector; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

- IT Glycolysis  
(partial blocking through PPP enzymes; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT Alcohols, preparation  
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)  
(polyhydric; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT *Saccharomyces cerevisiae*  
(redox enzymes of, expression in Pichia of **genes** for; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT *Klebsiella pneumoniae*  
(ribitol dehydrogenase **gene** of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(rpi, for D-ribose-phosphate isomerase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT Carbohydrates, preparation  
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)  
(sugar phosphates; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(tkt, for transketolase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(tsr, or fba, for aldolase; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT *Zymomonas mobilis*  
(zwf **gene** of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
(zwf, in regulation of PPP oxidative capacity; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 311826-80-9 311826-82-1 351916-74-0 351916-75-1 351916-76-2 351916-79-5  
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
(amino acid sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 351916-81-9 351916-83-1  
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)



- (amino acid sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 64-17-5P, Ethanol, preparation  
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)  
 (fermentation of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 50-99-7, D-Glucose, biological studies  
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
 (five carbon sugar or sugar alc. fermentation from; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 65187-56-6, 2-Deoxyglucose-6-phosphate phosphatase  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
 (**gene** DOG1; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 79747-53-8, Phosphatase, phosphoprotein (phosphotyrosine)  
 RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)  
 (**gene** PPPase1 or PPPase2; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 9001-46-1, NAD-dependent glutamate dehydrogenase  
 RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)  
 (**gene** for, of *Saccharomyces cerevisiae*, cloning and expression of; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 9028-18-6, Arabitol dehydrogenase  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
 (**gene** for; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 60063-83-4, L-Fucose isomerase  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
 (**gene** fucI; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 9001-40-5, Glucose-6-phosphate dehydrogenase 9001-82-5, 6-Phosphogluconate dehydrogenase  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
 (in regulation of PPP oxidative capacity; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 9001-36-9, Glucokinase 9001-41-6, Phosphoglucoisomerase 9001-51-8, Hexokinase 37278-03-8, Phosphofructokinase  
 RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)  
 (in regulation of glucose uptake and glucose carbon flow into PPP; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)
- IT 87-99-0P, Xylitol 488-81-3P, Ribitol 488-84-6P, D-Ribulose

551-84-8P, Xylulose 1114-34-7P, D-Lyxose 2152-56-9P, Arabitol  
 4151-19-3P, Ribulose-5-phosphate 4212-65-1P, Xylulose-5-phosphate  
 4300-28-1P, Ribose 5-phosphate 10323-20-3P, D-Arabinose  
 RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP  
 (Preparation)

(manufacture of five-carbon sugars and sugar alcs. using microorganisms  
 deficient in or transformed with **genes** involved in  
 pentose-phosphate pathway)

IT 58-86-6P, Xylose, biological studies

RL: BMF (Bioindustrial manufacture); BPR (Biological process); BSU  
 (Biological study, unclassified); BIOL (Biological study); PREP  
 (Preparation); PROC (Process)

(manufacture of five-carbon sugars and sugar alcs. using microorganisms  
 deficient in or transformed with **genes** involved in  
 pentose-phosphate pathway)

IT 53-57-6, NADPH 53-59-8, NADP 53-84-9, NAD 58-68-4, NADH 64-69-7  
 9001-50-7, Glyceraldehyde-3-phosphate dehydrogenase 79082-92-1,  
 Fructose-2,6-bisphosphate

RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL  
 (Biological study); PROC (Process)

(manufacture of five-carbon sugars and sugar alcs. using microorganisms  
 deficient in or transformed with **genes** involved in  
 pentose-phosphate pathway)

IT 9030-58-4, Xylulokinase 64886-68-6, Xylitol-phosphate  
 dehydrogenase

RL: BSU (Biological study, unclassified); BUU (Biological use,  
 unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)

(manufacture of five-carbon sugars and sugar alcs. using microorganisms  
 deficient in or transformed with **genes** involved in  
 pentose-phosphate pathway)

IT 9001-80-3, Kinase (phosphorylating), phosphofructo- 9014-23-7, Ribitol  
 dehydrogenase 9014-48-6, Transketolase 9023-83-0, Isomerase, ribose  
 phosphate 9024-20-8, D-Ribulose 5-phosphate Epimerase 9028-16-4  
 , Xylitol dehydrogenase 9031-25-8, D-Mannose  
 isomerase 99775-25-4, Xylose reductase

150316-09-9, D-Ketohexose 3-epimerase

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES  
 (Uses)

(manufacture of five-carbon sugars and sugar alcs. using microorganisms  
 deficient in or transformed with **genes** involved in  
 pentose-phosphate pathway)

IT 6917-36-8P, Pentitol

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP  
 (Preparation)

(manufacture of; manufacture of five-carbon sugars and sugar alcs. using  
 microorganisms deficient in or transformed with **genes**  
 involved in pentose-phosphate pathway)

IT 351916-80-8 351916-82-0

RL: BSU (Biological study, unclassified); BUU (Biological use,  
 unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)

(nucleotide sequence; manufacture of five-carbon sugars and sugar alcs.  
 using microorganisms deficient in or transformed with **genes**  
 involved in pentose-phosphate pathway)

IT 351916-77-3 351916-78-4

RL: BSU (Biological study, unclassified); BUU (Biological use,  
 unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)

(nucleotide sequences; manufacture of five-carbon sugars and sugar alcs.  
 using microorganisms deficient in or transformed with **genes**  
 involved in pentose-phosphate pathway)

IT 9024-52-6, Aldolase

RL: BUU (Biological use, unclassified); BIOL (Biological study); USES  
 (Uses)

(promoter from the **gene** for; manufacture of five-carbon sugars and

sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 9028-46-0, Malic enzyme 9028-86-8, Aldehyde dehydrogenase  
**104118-53-8, Xylose reductase**  
 RL: BPR (Biological process); BSU (Biological study, unclassified); CAT (Catalyst use); BIOL (Biological study); PROC (Process); USES (Uses)  
 (redox system using; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351919-59-0 351919-60-3 351919-61-4 351919-62-5 351919-63-6  
 351919-64-7 351919-65-8 351919-66-9 351919-67-0 351919-68-1  
 351919-69-2 351919-70-5 351919-71-6 351919-72-7 351919-73-8  
 351919-74-9 351919-75-0 351919-76-1 351919-77-2 351919-78-3  
 351919-79-4 351919-80-7 351919-81-8 351919-82-9 351919-83-0  
 351919-84-1 351919-85-2 351919-86-3 351919-87-4 351919-88-5  
 351919-89-6 351919-90-9 351919-91-0 351919-92-1 351919-93-2  
 351919-94-3 351919-95-4 351919-96-5 351919-98-7 351920-00-8  
 351920-01-9 351920-03-1 351920-04-2 351920-05-3 351920-06-4  
 351920-07-5 351920-08-6 351920-09-7 351920-10-0 351920-11-1, 1:  
 PN: WO0153306 SEQID: 1 unclaimed **DNA**  
 RL: PRP (Properties)  
 (unclaimed nucleotide sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351919-99-8  
 RL: PRP (Properties)  
 (unclaimed protein sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

IT 351900-48-6 351900-49-7 351900-50-0 351900-51-1 351900-52-2  
 351900-53-3 351900-54-4 351900-55-5  
 RL: PRP (Properties)  
 (unclaimed sequence; manufacture of five-carbon sugars and sugar alcs. using microorganisms deficient in or transformed with **genes** involved in pentose-phosphate pathway)

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 PA Purdue Research Foundation, USA; Ho, Nancy W. Y.; Chen, Zheng-Dao  
 SO PCT Int. Appl., 66 pp.  
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| WO 9742307  | A1   | 19971113 | WO 1997-US7663  | 19970506 <-- |
| W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM |      |          |                 |              |
| RW: GH, KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN,   |      |          |                 |              |

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ML, MR, NE, SN, TD, TG

|   |    |              |                |              |
|---|----|--------------|----------------|--------------|
| AU 9728301  | A1 | 19971126     | AU 1997-28301  | 19970506 <-- |
| AU 731102   | B2 | 20010322     |                |              |
| EP 898616   | A1 | 19990303     | EP 1997-922698 | 19970506 <-- |
| R: AT, BE, DE, DK, ES, FR, GB, GR, IT, NL, SE, PT, IE, FI |    |              |                |              |
| CN 1225125  | A  | 19990804     | CN 1997-196195 | 19970506 <-- |
| JP 2000509988   | T2 | 20000808     | JP 1997-540153 | 19970506 <-- |
| BR 9710963  | A  | 20010731     | BR 1997-10963  | 19970506 <-- |
| PRAI US 1996-16865P                                       | P  | 19960506 <-- |                |              |
| WO 1997-US7663  | W  | 19970506 <-- |                |              |

AB Described are recombinant **yeast** which ferment xylose to EtOH and which maintain their ability to do so when cultured for numerous generations in non-selective media. The preferred **yeast** contain multiple copies of integrated **genes** encoding **xylose reductase, xylitol dehydrogenase**, and **xylulokinase** fused to promoters which are non-glucose inhibited and which do not require xylose for induction. Also described are preferred methods for integrating multiple copies of exogenous **DNA** into host cells by transforming cells with replicative/integrative vectors, and then replicating the cells a number of times under selective pressure to promote retention of the vector in subsequent generations. The replicated vectors thus serve to integrate multiple copies of the exogenous **DNA** into the host cells throughout the replication/selection phase. Thereafter the selective pressure can be removed to promote loss of the vector in subsequent generations, leaving stable integrants of the exogenous **DNA**.

ST Saccharomyces recombinant ethanol ferment xylose

IT Genetic engineering

**Saccharomyces cerevisiae**  
(stable recombinant **yeasts** for fermenting xylose to ethanol)

IT 64-17-5P, Ethanol, preparation  
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)  
(stable recombinant **yeasts** for fermenting xylose to ethanol)

IT 9028-16-4, **Xylitol dehydrogenase**  
9030-58-4, **Xylulokinase** 99775-25-4,  
**Xylose reductase**  
RL: BOC (Biological occurrence); BPR (Biological process); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); OCCU (Occurrence); PROC (Process); USES (Uses)  
(stable recombinant **yeasts** for fermenting xylose to ethanol)

IT 58-86-6, D-Xylose, biological studies  
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)  
(stable recombinant **yeasts** for fermenting xylose to ethanol)

L49 ANSWER 5 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 1997:464186 HCAPLUS

DN 127:94156

ED Entered STN: 24 Jul 1997

TI Fermentation of corn fiber sugars by an engineered xylose utilizing Saccharomyces **yeast** strain

AU Moniruzzaman, M.; Dien, B.S.; Skory, C.D.; **Chen, Z.D.**; Hespell, R.B.; **Ho, N.W.Y.**; Dale, B.E.; Bothast, R.J.

CS Department of Chemical Engineering, Texas AandM University, College Station, TX, 77843, USA

SO World Journal of Microbiology & Biotechnology (1997), 13(3), 341-346  
CODEN: WJMBEY; ISSN: 0959-3993

PB Rapid Science Publishers

DT Journal

LA English

CC 16-5 (Fermentation and Bioindustrial Chemistry)

- AB The ability of a recombinant *Saccharomyces yeast* strain to ferment the sugars glucose, xylose, arabinose and galactose which are the predominant monosaccharides found in corn fiber hydrolyzates has been examined. *Saccharomyces* strain 1400 (pLNH32) was genetically engineered to ferment xylose by expressing **genes** encoding a **xylose reductase**, a **xylitol dehydrogenase** and a **xylulose kinase**. The recombinant efficiently fermented xylose alone or in the presence of glucose. Xylose-grown cultures had very little difference in xylitol accumulation, with only 4 to 5 g/L accumulating, in aerobic, micro-aerated and anaerobic conditions. Highest production of ethanol with all sugars was achieved under anaerobic conditions. From a mixture of glucose (80 g/L) and xylose (40 g/L), this strain produced 52 g/L ethanol, equivalent to 85% of theor. yield, in less than 24 h. Using a mixture of glucose (31 g/L), xylose (15.2 g/L), arabinose (10.5 g/L) and galactose (2 g/L), all of the sugars except arabinose were consumed in 24 h with an accumulation of 22 g ethanol/L, a 90% yield (excluding the arabinose in the calcn. since it is not fermented). Approx. 98% theor. yield, or 21 g ethanol/L, was achieved using an enzymic hydrolyzate of ammonia fiber exploded corn fiber containing an estimated 47.0 g mixed sugars/L.
- In all mixed sugar fermns., less than 25% arabinose was consumed and converted into arabitol.
- ST corn fiber sugar fermn *Saccharomyces xylose*; ethanol fermn corn fiber **xylose yeast**
- IT Fermentation  
(fermentation of corn fiber sugars by engineered xylose utilizing *Saccharomyces yeast* strain)
- IT Carbohydrates, biological studies  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(fermentation of corn fiber sugars by engineered xylose utilizing *Saccharomyces yeast* strain)
- IT Corn  
(fiber; fermentation of corn fiber sugars by engineered xylose utilizing *Saccharomyces yeast* strain)
- IT 64-17-5P, Ethanol, preparation  
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)  
(fermentation; fermentation of corn fiber sugars by engineered xylose utilizing *Saccharomyces yeast* strain)
- IT 50-99-7, Glucose, biological studies 58-86-6, Xylose, biological studies 59-23-4, Galactose, biological studies 147-81-9, Arabinose  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(fermentation of corn fiber sugars by engineered xylose utilizing *Saccharomyces yeast* strain)
- L49 ANSWER 6 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
- AN 1996:671095 HCAPLUS
- DN 126:2045
- ED Entered STN: 13 Nov 1996
- TI **Yeast** Sequencing Reports: Sequence and analysis of an aldose ( **xylose**) **reductase gene** from the xylose-fermenting **yeast** *Pachysolen tannophilus*
- AU Bolen, Paul L.; Hayman, G. Thomas; Shepherd, Hurley S.
- CS Microbial Properties Res., National Center Agricultural Utilization Res., Agricultural Res. Serv., U.S. Dep. Agriculture, Peoria, IL, 61604, USA
- SO *Yeast* (1996), 12(13), 1367-1375  
CODEN: YESTE3; ISSN: 0749-503X
- PB Wiley
- DT Journal
- LA English
- CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 7, 10

- AB A **xylose reductase gene** was isolated from the xylose-fermenting yeast *Pachysolen tannophilus* as a cDNA clone by selecting clones that hybridized specifically to xylose-inducible mRNA. Use of the cDNA clone as a probe in Northern hybridizations identified a xylose-inducible mRNA. Use of the cDNA clone as a probe in Northern hybridizations identified a xylose-inducible mRNA species large enough to encode a 36 kDa **xylose reductase** protein known to be produced by this yeast. A corresponding genomic clone was isolated as a 3 kb EcoRI fragment that specifically hybridized to the cDNA clone. The sequence of the cDNA and the largest open reading frame of the genomic clone are identical. The predicted translation product exhibits: (1) significant sequence identity with a previously published N-terminal amino acid sequence from purified *P. tannophilus* **xylose (aldose) reductase** protein exhibiting NADH/NADHP-dependent activities (**aldose reductase**, EC 1.1.1.21); (2) identity with a protein composed of 317 amino acid residues with a calculated mol. mass of 36.2 kDa, equivalent to that reported for purified *P. tannophilus* **xylose reductase**; and (3) considerable sequence similarity to, and features of, a superfamily of oxidoreductases. This sequence is deposited as GenBank Accession Number U40706.
- ST DNA sequence *Pachysolen* **aldose reductase gene**; **aldose reductase** protein sequence  
*Pachysolen*
- IT DNA sequences  
*Pachysolen tannophilus*  
Protein sequences  
cDNA sequences  
(sequence and anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting yeast *Pachysolen tannophilus*)
- IT 183327-22-2  
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)  
(amino acid sequence; anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting yeast *Pachysolen tannophilus*)
- IT 58-86-6, Xylose, biological studies  
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)  
(anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting yeast *Pachysolen tannophilus*)
- IT 183399-64-6  
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)  
(nucleotide sequence; anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting yeast *Pachysolen tannophilus*)
- IT 9028-31-3, **Aldose reductase**  
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)  
(sequence and anal. of an aldose (**xylose**) **reductase gene** from the xylose-fermenting yeast *Pachysolen tannophilus*)

L49 ANSWER 7 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 1996:606013 HCAPLUS

DN 125:270220

ED Entered STN: 11 Oct 1996

TI A glycerol-3-phosphate dehydrogenase-deficient mutant of *Saccharomyces cerevisiae* expressing the heterologous XYL1 **gene**

AU Liden, G.; Walfridsson, M.; Ansell, R.; Anderlund, M.; Adler, L.;

- Hahn-Haegerdal, B.  
 CS Dep. Chem. Reaction Eng., Chalmers Univ. Technol., Goeteborg, S-412 96, Swed.  
 SO Applied and Environmental Microbiology (1996), 62(10), 3894-3896  
 CODEN: AEMIDF; ISSN: 0099-2240  
 PB American Society for Microbiology  
 DT Journal  
 LA English  
 CC 10-4 (Microbial, Algal, and Fungal Biochemistry)  
 Section cross-reference(s): 3  
 AB The **gene** *XYL1*, encoding a **xylose reductase**, from *Pichia stipitis* was transformed into a mutant of *Saccharomyces cerevisiae* incapable of glycerol production because of deletion of the **genes** *GPD1* and *GPD2*. The transformed strain was capable of anaerobic glucose conversion in the presence of added xylose, indicating that the **xylose reductase** reaction can fulfill the role of the glycerol-3-phosphate dehydrogenase reaction as a redox sink. The specific xylitol production rate obtained was 0.38 g g<sup>-1</sup> h<sup>-1</sup>.  
 ST *Pichia xylose reductase gene* cloning  
*Saccharomyces*; **yeast gene** *XYL1* cloning glycerol dehydrogenase  
 IT Molecular cloning  
     *Saccharomyces cerevisiae*  
     *Yamadazyma stipitis*  
     (glycerol-3-phosphate dehydrogenase-deficient mutant of *Saccharomyces cerevisiae* expressing heterologous *XYL1 gene*)  
 IT **Gene**, microbial  
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
     (*XYL1*, glycerol-3-phosphate dehydrogenase-deficient mutant of *Saccharomyces cerevisiae* expressing heterologous *XYL1 gene*)  
 IT 9075-65-4, Glycerol-3-phosphate dehydrogenase  
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)  
     (glycerol-3-phosphate dehydrogenase-deficient mutant of *Saccharomyces cerevisiae* expressing heterologous *XYL1 gene*)  
 IT **95829-40-6, Xylose reductase**  
 RL: BSU (Biological study, unclassified); BIOL (Biological study)  
     (glycerol-3-phosphate dehydrogenase-deficient mutant of *Saccharomyces cerevisiae* expressing heterologous *XYL1 gene*)
- L49 ANSWER 8 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1996:308481 HCAPLUS  
 DN 124:340999  
 ED Entered STN: 25 May 1996  
 TI A metabolic engineering view on molecular breeding of an alcohol fermenting **yeast** from xylose  
 AU Seki, Tatsuji; Tantirungkij, Manee; Fujiyama, Kazuhito; Yoshida, Toshiomi  
 CS International Center Cooperative Research Biotechnology, Osaka University, Suita, 565, Japan  
 SO Environmental Biotechnology: Principles and Applications, [Papers presented at the International Symposium on Environmental Biotechnology], Waterloo, Ont., July 4-8, 1994 (1996), Meeting Date 1994, 114-124. Editor(s): Moo-Young, Murray; Anderson, William A.; Chakrabarty, Ananda M. Publisher: Kluwer, Dordrecht, Neth.  
 CODEN: 62UGA4  
 DT Conference  
 LA English  
 CC 16-5 (Fermentation and Bioindustrial Chemistry)  
 Section cross-reference(s): 3  
 AB Xylose-assimilating *S. cerevisiae* was constructed by introducing the **xylose reductase** and **xylitol dehydrogenase genes** originating from *P. stipitis*. Good

growth of the transformant in xylose medium was observed under aerobic conditions. Under a limited oxygen condition, the transformant produced a lesser amount of ethanol than *P. stipitis*, and a remarkable amount of xylitol was accumulated. A mutant, IM2, in which the ratio of **xylose reductase** to **xylitol dehydrogenase** activities was lower than the parental strain, exhibited an improved fermentation with

less

accumulation of xylitol and a higher yield. The limited feeding of xylose could also improve the fermentation, with reduced xylitol accumulation as well as increased ethanol yield. The facts suggest strongly that the path of the conversion from xylitol to xylulose is the "bottleneck" due to a poor regeneration of NAD essential for the conversion. An appropriate oxygen supply also improved the ethanol production and the production rate,

suggesting it

may contribute to the NAD recycle from NADH.

ST ethanol manuf *Saccharomyces xylose*

IT Fermentation

Genetic engineering

***Saccharomyces cerevisiae***

(genetic engineering of **yeast** for ethanol fermentation from xylose)

IT 58-86-6, Xylose, biological studies

RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)

(genetic engineering of **yeast** for ethanol fermentation from xylose)

IT 64-17-5P, Ethanol, preparation

RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)

(genetic engineering of **yeast** for ethanol fermentation from xylose)

IT 87-99-0P, Xylitol

RL: BYP (Byproduct); PREP (Preparation)

(genetic engineering of **yeast** for ethanol fermentation from xylose)

L49 ANSWER 9 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 1996:158446 HCAPLUS

DN 124:252209

ED Entered STN: 19 Mar 1996

TI Sequencing and analysis of 51 kb on the right arm of **chromosome** XV from *Saccharomyces cerevisiae* reveals 30 open reading frames

AU Wieman, Stefan; Rechmann, Stefanie; Benes, Vladimir; Voss, Hartmut; Schwager, Christian; Vlcek, Cestmir; Stegemann, Josef; Zimmermann, Jurgen; Erfle, Holger; et al.

CS EMBL, Heidelberg, D-69117, Germany

SO Yeast (1996), 12(3), 281-8

CODEN: YESTE3; ISSN: 0749-503X

PB Wiley

DT Journal

LA English

CC 3-3 (Biochemical Genetics)

AB We have sequenced a region of 51 kb of the right arm from **chromosome** XV of *Saccharomyces cerevisiae*. The sequence contains 30 open reading frames (ORFs) of more than 100 amino acid residues. Thirteen new **genes** have been identified. Thirteen ORFs correspond to known **yeast genes**. One delta element and one tRNA **gene** were identified. Upstream of the RPO31 **gene**, encoding the largest subunit of RNA polymerase III, lies a Abfp binding site. The nucleotide sequence data reported in this paper are available in the EMBL, GenBank and DDBJ nucleotide sequence databases under the Accession Number X90518.

ST *Saccharomyces chromosome* XV **gene** sequence

IT Deoxyribonucleic acid sequences

Protein sequences

***Saccharomyces cerevisiae***

(sequencing and anal. of 51 kb on right arm of **chromosome** XV)



- from *Saccharomyces cerevisiae* reveals 30 open reading frames)
- IT **Gene**, microbial  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(sequencing and anal. of 51 kb on right arm of **chromosome XV**  
from *Saccharomyces cerevisiae* reveals 30 open reading frames)
- IT **Chromosome**  
(*Saccharomyces cerevisiae* XV, sequencing and anal. of 51 kb on right  
arm of **chromosome XV** from *Saccharomyces cerevisiae* reveals 30  
open reading frames)
- IT Ribonucleic acids, transfer  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(aspartic acid-specific, **gene** for; sequencing and anal. of 51  
kb on right arm of **chromosome XV** from *Saccharomyces*  
*cerevisiae* reveals 30 open reading frames)
- IT Protein formation elongation factors  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(eEF-2, **gene** for; sequencing and anal. of 51 kb on right arm  
of **chromosome XV** from *Saccharomyces cerevisiae* reveals 30  
open reading frames)
- IT 9014-24-8  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(III, **gene** for; sequencing and anal. of 51 kb on right arm of  
**chromosome XV** from *Saccharomyces cerevisiae* reveals 30 open  
reading frames)
- IT **121548-71-8**, Protein (*Saccharomyces cerevisiae* **gene** GCY  
reduced) **122178-43-2**, Profilin (*Saccharomyces cerevisiae* **gene**  
PFY) **133758-72-2** **146313-69-1**, Protein formation elongation factor EF 2  
(*Saccharomyces cerevisiae* strain YM213 **gene** EFT1 reduced)  
**156656-75-6** **157712-16-8** **159521-43-4** **172929-93-0** **172929-97-4**  
**174763-93-0** **174763-94-1** **174763-95-2** **174763-96-3** **174763-97-4**  
**174763-98-5** **174763-99-6** **174764-00-2** **174764-01-3** **174764-02-4**  
**174764-03-5** **174764-04-6** **174764-05-7** **174764-06-8**  
RL: PRP (Properties)  
(amino acid sequence; sequencing and anal. of 51 kb on right arm of  
**chromosome XV** from *Saccharomyces cerevisiae* reveals 30 open  
reading frames)
- IT **86480-67-3**  
RL: BSU (Biological study, unclassified); BIOL (Biological study)  
(**gene** for; sequencing and anal. of 51 kb on right arm of  
**chromosome XV** from *Saccharomyces cerevisiae* reveals 30 open  
reading frames)
- IT **170321-17-2**, GenBank X90518  
RL: PRP (Properties)  
(nucleotide sequence; sequencing and anal. of 51 kb on right arm of  
**chromosome XV** from *Saccharomyces cerevisiae* reveals 30 open  
reading frames)
- L49 ANSWER 10 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1995:814692 HCAPLUS  
DN 124:2028  
ED Entered STN: 27 Sep 1995  
TI Isolation and characterization of the **gene** encoding  
**xylose reductase** from *Kluyveromyces lactis*  
AU Billard, Patrick; Menart, Sandrine; Fleer, Reinhard; Bolotin-Fukuhara,  
Monique  
CS Institut de Genetique et Microbiologie, Bat. 400, Universite Paris-Sud,  
91405, Orsay, Fr.  
SO Gene (1995), 162(1), 93-7  
CODEN: GENED6; ISSN: 0378-1119  
PB Elsevier  
DT Journal  
LA English  
CC 3-3 (Biochemical Genetics)

Section cross-reference(s): 7, 10

- AB The identification of a **xylose reductase** (XR)-encoding **gene** (XYL1) from the xylose-assimilating **yeast** *Kluyveromyces lactis* (Kl) is described. XYL1 was isolated as a highly expressed fusion clone from a 'lacZ translational fusion library. DNA sequence anal. revealed an open reading frame (ORF) of 987bp capable of encoding a polypeptide of 329 amino acids (aa). The deduced aa sequence displays a 62% overall identity to that of XR from *Pichia stipitis*. **Gene** disruption studies indicate that XYL1 exists as a single copy in the **yeast** genome and is essential for growth on xylose. Northern blot anal. of the XYL1 transcript and measurement of the XR enzymic activities show, in contrast to other known XR-encoding **genes**, a constitutive expression of Kl XYL1.
- ST *Kluyveromyces xylose reductase gene* sequence; XYL1 **gene** *Kluyveromyces xylose reductase* sequence
- IT *Kluyveromyces lactis*  
(isolation and characterization of **gene** encoding **xylose reductase** from *Kluyveromyces lactis*)
- IT Deoxyribonucleic acid sequences  
(of **gene** XYL1 from *Kluyveromyces lactis*)
- IT Protein sequences  
(of **xylose reductase** from *Kluyveromyces lactis*)
- IT **Gene**, microbial  
RL: PRP (Properties)  
(XYL1, isolation and characterization of **gene** encoding **xylose reductase** from *Kluyveromyces lactis*)
- IT 171043-09-7  
RL: PRP (Properties)  
(amino acid sequence; isolation and characterization of **gene** encoding **xylose reductase** from *Kluyveromyces lactis*)
- IT 58-86-6, Xylose, biological studies  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(isolation and characterization of **gene** encoding **xylose reductase** from *Kluyveromyces lactis*)
- IT 104118-53-8, **Xylose reductase**  
RL: PRP (Properties)  
(isolation and characterization of **gene** encoding **xylose reductase** from *Kluyveromyces lactis*)
- IT 158764-02-4, GenBank L36993  
RL: PRP (Properties)  
(nucleotide sequence; isolation and characterization of **gene** encoding **xylose reductase** from *Kluyveromyces lactis*)
- IT 53-57-6, NADPH  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(**xylose reductase** from *Kluyveromyces lactis* dependence on NADPH)
- L49 ANSWER 11 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN
- AN 1995:756362 HCAPLUS
- DN 123:196764
- ED Entered STN: 25 Aug 1995
- TI Recombinant **yeasts** for effective fermentation of glucose and xylose
- IN **Ho, Nancy W. Y.**; Tsao, George T.
- PA Purdue Research Foundation, USA
- SO PCT Int. Appl., 62 pp.
- CODEN: PIXXD2
- DT Patent

LA English  
 IC ICM C12N001-14  
 ICS C12N009-00; C12N009-12; C12N015-00; C12P007-08  
 CC 16-5 (Fermentation and Bioindustrial Chemistry)  
 FAN.CNT 2

|      | PATENT NO.   | KIND | DATE     | APPLICATION NO. | DATE         |
|------|--|------|----------|-----------------|--------------|
| PI   | WO 9513362   | A1   | 19950518 | WO 1994-US12861 | 19941108 <-- |
|      | W: AM, AU, BB, BG, BR, BY, CA, CN, CZ, EE, FI, GE, HU, JP, KG, KP, KR, KZ, LK, LR, LT, LV, MD, MG, MN, NO, NZ, PL, RO, RU, SI, SK, TJ, TT, UA, UZ, VN  |      |          |                 |              |
|      | RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG   |      |          |                 |              |
|      | US 5789210   | A    | 19980804 | US 1993-148581  | 19931108 <-- |
|      | CA 2176038   | AA   | 19950518 | CA 1994-2176038 | 19941108 <-- |
|      | AU 9510517   | A1   | 19950529 | AU 1995-10517   | 19941108 <-- |
|      | AU 695930  | B2   | 19980827 |                 |              |
|      | EP 728192  | A1   | 19960828 | EP 1995-901176  | 19941108 <-- |
|      | R: AT, BE, DE, DK, ES, FR, GB, GR, IE, IT, NL, SE  |      |          |                 |              |
|      | BR 9408010   | A    | 19961217 | BR 1994-8010    | 19941108 <-- |
|      | CN 1141057   | A    | 19970122 | CN 1994-194767  | 19941108 <-- |
|      | CN 1128873   | B    | 20031126 |                 |              |
|      | JP 09505469  | T2   | 19970603 | JP 1994-513948  | 19941108 <-- |
|      | PL 176399  | B1   | 19990531 | PL 1994-314297  | 19941108 <-- |
|      | FI 9601926   | A    | 19960704 | FI 1996-1926    | 19960507 <-- |
| PRAI | US 1993-148581   | A    | 19931108 | <--             |              |
|      | US 1993-148541   | A    | 19931108 | <--             |              |
|      | WO 1994-US12861  | W    | 19941108 | <--             |              |
| AB   | Described are recombinant <b>yeasts</b> containing <b>genes</b> encoding <b>xylose reductase</b> , <b>xylitol dehydrogenase</b> and <b>xylulokinase</b> , and <b>DNA</b> mols., vectors and methods useful for producing such <b>yeasts</b> . The recombinant <b>yeasts</b> effectively ferment xylose to EtOH, and preferred <b>yeasts</b> are capable of simultaneously fermenting glucose and xylose to EtOH, thereby taking full advantage of these 2 sugar sources as they are found in agricultural biomass. |      |          |                 |              |
| ST   | recombinant <b>yeast</b> ethanol fermn glucose xylose  |      |          |                 |              |
| IT   | Deoxyribonucleic acid sequences<br>(for <b>xylulokinase gene</b> of <i>Saccharomyces cerevisiae</i> )  |      |          |                 |              |
| IT   | Protein sequences<br>(for <b>xylulokinase</b> of <i>Saccharomyces cerevisiae</i> )   |      |          |                 |              |
| IT   | Fermentation<br><b>Saccharomyces cerevisiae</b><br>(recombinant <b>yeasts</b> for effective fermentation of glucose and xylose)  |      |          |                 |              |
| IT   | <b>Gene</b> , microbial<br>RL: PRP (Properties)<br>( <b>xylulokinase</b> ; sequence of <b>xylulokinase gene</b> of <i>Saccharomyces cerevisiae</i> )   |      |          |                 |              |
| IT   | <b>167078-89-9</b><br>RL: PRP (Properties)<br>(amino acid sequence; recombinant <b>yeasts</b> for effective fermentation of glucose and xylose)  |      |          |                 |              |
| IT   | <b>167974-35-8</b><br>RL: PRP (Properties)<br>(nucleotide sequence; recombinant <b>yeasts</b> for effective fermentation of glucose and xylose)  |      |          |                 |              |
| IT   | <b>9028-16-4, Xylitol dehydrogenase</b><br><b>9030-58-4, Xylulokinase</b> 99775-25-4,<br><b>Xylose reductase</b><br>RL: CAT (Catalyst use); USES (Uses)<br>(recombinant <b>yeasts</b> containing cloned enzyme <b>genes</b> for  |      |          |                 |              |

- effective fermentation of glucose and xylose)
- IT 64-17-5P, Ethanol, preparation  
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)  
(recombinant **yeasts** for effective fermentation of glucose and xylose)
- IT 50-99-7, Glucose, biological studies 58-86-6, Xylose, biological studies  
RL: BPR (Biological process); BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological study); PROC (Process); RACT (Reactant or reagent)  
(recombinant **yeasts** for effective fermentation of glucose and xylose)
- L49 ANSWER 12 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1994:650857 HCAPLUS  
DN 121:250857  
ED Entered STN: 26 Nov 1994  
TI Utilization of xylose with recombinant *Saccharomyces cerevisiae* harboring **genes** for xylose metabolism from *Pichia stipitis*  
AU Meinander, Nina; Hallborn, Johan; Keranen, Sirkka; Ojamo, Heikki; Penttila, Merja; Walfridsson, Mats; Hahn-Haegerdal, Barbel  
CS Chemical center, University Lund, Lund, S-22100, Swed.  
SO Progress in Biotechnology (1994), 9 (ECB6: PROCEEDINGS OF THE 6TH EUROPEAN CONGRESS ON BIOTECHNOLOGY, 1993, PT. 2), 1143-6  
CODEN: PBITE3; ISSN: 0921-0423  
DT Journal  
LA English  
CC 10-2 (Microbial, Algal, and Fungal Biochemistry)  
Section cross-reference(s): 3  
AB Normally, *S. cerevisiae* lacks the enzymes necessary to convert xylose into xylulose and is thereby unable to utilize xylose in its metabolism. An *S. cerevisiae* strain expressing both the **xylose reductase** (converting xylose to xylitol) and **xylitol dehydrogenase** (converting xylitol to xylulose) **genes** of *P. stipitis* was constructed. This strain was able to grow on and ferment xylose.  
ST xylose metab *Saccharomyces* recombinant  
IT Molecular cloning  
*Pichia stipitis*  
***Saccharomyces cerevisiae***  
(xylose utilization by recombinant *Saccharomyces cerevisiae* harboring **genes** for xylose metabolism from *Pichia stipitis*)  
IT **Gene**, microbial  
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)  
(xylose utilization by recombinant *Saccharomyces cerevisiae* harboring **genes** for xylose metabolism from *Pichia stipitis*)  
IT 9028-16-4, **Xylitol dehydrogenase**  
95829-40-6, **Xylose reductase**  
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)  
(xylose utilization by recombinant *Saccharomyces cerevisiae* harboring **genes** for xylose metabolism from *Pichia stipitis*)  
IT 58-86-6, Xylose, biological studies  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(xylose utilization by recombinant *Saccharomyces cerevisiae* harboring **genes** for xylose metabolism from *Pichia stipitis*)
- L49 ANSWER 13 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1994:650854 HCAPLUS  
DN 121:250854  
ED Entered STN: 26 Nov 1994  
TI Bioconversion of xylose to xylitol with in situ generation of NAD(P)H in

recombinant *Saccharomyces cerevisiae*  
 AU Carlsen, Helle N.; Hallborn, Johan; Gorwa, Marie-Francoise;  
 Hahn-Haegerdal, Baerbel  
 CS Chemical Center, University Lund, Lund, S-221 00, Swed.  
 SO Progress in Biotechnology (1994), 9(ECB6: PROCEEDINGS OF THE 6TH  
 EUROPEAN CONGRESS ON BIOTECHNOLOGY, 1993, PT. 1), 313-16  
 CODEN: PBITE3; ISSN: 0921-0423  
 DT Journal  
 LA English  
 CC 10-2 (Microbial, Algal, and Fungal Biochemistry)  
 Section cross-reference(s): 3  
 AB The **xylose reductase gene** of *Pichia stipitis*  
 was cloned into *S. cerevisiae*. The recombinant *S. cerevisiae* was thus  
 able to convert xylose to xylitol. The cofactor NAD(P)H, used for xylose  
 reduction, could be generated in situ through the oxidation of ethanol,  
 acetate,  
 or glucose.  
 ST xylose metab *Saccharomyces* recombinant  
 IT Molecular cloning  
     *Saccharomyces cerevisiae*  
     (bioconversion of xylose to xylitol with in situ generation of NAD(P)H  
     in recombinant *Saccharomyces cerevisiae*)  
 IT 58-86-6, Xylose, biological studies  
 RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL  
 (Biological study); PROC (Process)  
     (bioconversion of xylose to xylitol with in situ generation of NAD(P)H  
     in recombinant *Saccharomyces cerevisiae*)  
 IT 53-57-6, NADPH 58-68-4, NADH  
 RL: BPR (Biological process); BSU (Biological study, unclassified); MFM  
 (Metabolic formation); BIOL (Biological study); FORM (Formation,  
 nonpreparative); PROC (Process)  
     (bioconversion of xylose to xylitol with in situ generation of NAD(P)H  
     in recombinant *Saccharomyces cerevisiae*)  
 IT 87-99-0, Xylitol  
 RL: BSU (Biological study, unclassified); MFM (Metabolic formation); BIOL  
 (Biological study); FORM (Formation, nonpreparative)  
     (bioconversion of xylose to xylitol with in situ generation of NAD(P)H  
     in recombinant *Saccharomyces cerevisiae*)  
 L49 ANSWER 14 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1994:532375 HCAPLUS  
 DN 121:132375  
 ED Entered STN: 17 Sep 1994  
 TI Manufacture of xylitol from carbon sources other than xylose or xylulose  
 using **yeasts** expressing foreign **genes**  
 IN Harkki, Anu Marjukka; Myasnikov, Andrey Novomirovich; Apajalahti, Juha  
 Heikki Antero; Pastinen, Ossi Antero  
 PA Xyrofin Oy, Finland  
 SO PCT Int. Appl., 90 pp.  
 CODEN: PIXXD2  
 DT Patent  
 LA English  
 IC ICM C12P007-18  
 ICS C12N015-52  
 CC 16-2 (Fermentation and Bioindustrial Chemistry)  
 Section cross-reference(s): 10, 17  
 FAN.CNT 3

|    | PATENT NO. | KIND   | DATE     | APPLICATION NO. | DATE         |
|----|------------|--|----------|-----------------|--------------|
| PI | WO 9410325 | A1   | 19940511 | WO 1993-FI450   | 19931105 <-- |
|    | W:         | AT, AU, BB, BG, BR, BY, CA, CH, CZ, DE, DK, ES, FI, GB, HU, JP, KP, KR, KZ, LK, LU, LV, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SK, UA, US, UZ, VN |          |                 |              |

RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,  
 BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

|   |    |          |                |              |
|---|----|----------|----------------|--------------|
| AU 9454215  | A1 | 19940524 | AU 1994-54215  | 19931105 <-- |
| EP 672161   | A1 | 19950920 | EP 1993-924615 | 19931105 <-- |
| EP 672161   | B1 | 19990922 |                |              |
| R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, PT, SE |    |          |                |              |
| HU 72187  | A2 | 19960328 | HU 1995-1288   | 19931105 <-- |
| HU 219016   | B  | 20010129 |                |              |
| JP 08505522   | T2 | 19960618 | JP 1994-510748 | 19931105 <-- |
| JP 3433295  | B2 | 20030804 |                |              |
| BR 9307391  | A  | 19990831 | BR 1993-7391   | 19931105 <-- |
| AT 184917   | E  | 19991015 | AT 1993-924615 | 19931105 <-- |
| RU 2142999  | C1 | 19991220 | RU 1995-113172 | 19931105 <-- |
| ES 2139024  | T3 | 20000201 | ES 1993-924615 | 19931105 <-- |
| PL 178040   | B1 | 20000229 | PL 1993-308742 | 19931105 <-- |
| FI 9502148  | A  | 19950704 | FI 1995-2148   | 19950504 <-- |
| NO 9501747  | A  | 19950705 | NO 1995-1747   | 19950504 <-- |
| PRAI US 1992-973325   | A  | 19921105 | <--            |              |
| US 1993-110672  |    | 19930824 | <--            |              |
| WO 1993-FI450   | W  | 19931105 | <--            |              |

AB Novel methods for the fermentation of xylitol from sugars using a **yeast** with modified D-arabitol metabolism are described. **Yeasts** synthesizing D-arabitol were modified by the introduction of expression cassettes for D-arabitol dehydrogenase and **xylitol dehydrogenase** and by inactivation of the host **genes** for transketolase and D-**xylulokinase** and increasing levels of expression of **genes** for enzymes of the oxidative branch of the pentose phosphate pathway. **Plasmid** pSRT(AX)-9 carrying expression cassettes for D-arabitol dehydrogenase and **xylitol dehydrogenase** was introduced into *Zygosaccharomyces rouxii*. Transformants showing significant activities of the 2 enzymes were used to manufacture xylitol with yields of 7.7 g/L obtained after 48 h. Yields depended upon nutritional conditions with higher yields coming from a medium enriched with **yeast** extract

ST xylitol ferment transgenic **yeast**; arabitol metab xylitol ferment **yeast**; pentose phosphate pathway xylitol ferment **yeast**

IT **Gene**, microbial  
 RL: BIOL (Biological study)  
 (XYL2, for **xylitol dehydrogenase** of *Pichia stipitis*, cloning and expression of, xylitol manufacture in fungi with altered arabitol metabolism in relation to)

IT **Gene**, microbial  
 RL: BIOL (Biological study)  
 (for transketolase of *Saccharomyces cerevisiae*, cloning and inactivation of, xylitol manufacture in relation to)

IT **Gene**, microbial  
 RL: BIOL (Biological study)  
 (for D-arabitol dehydrogenase of *Klebsiella terrigena*, cloning and expression of, xylitol manufacture in fungi with altered arabitol metabolism in relation to)

IT Pentose phosphate pathway  
 (oxidative branch of, increasing activity of, in xylitol manufacture with fungi with altered arabitol metabolism)

IT **Plasmid** and Episome  
 (pCPU(AX), **genes** for D-arabitol dehydrogenase and **xylitol dehydrogenase** on, expression in *Candida polymorpha* of, altered arabitol metabolism and xylitol manufacture in relation to)

IT **Plasmid** and Episome  
 (pSRT(AX)-9, **genes** for D-arabitol dehydrogenase and **xylitol dehydrogenase** on, expression in

- Zygosaccharomyces rouxii of, altered arabitol metabolism and xylitol manufacture in relation to)
- IT **Plasmid and Episome**  
(pSRT(ZG), **genes** for D-glucose-6-phosphate dehydrogenase and 6-phospho-D-gluconate dehydrogenase on, expression in Zygosaccharomyces rouxii of)
- IT **Plasmid and Episome**  
(pTC(AX), integrating dominant selection vector for Torulopsis candida, **genes** for D-arabitol dehydrogenase and **xylitol dehydrogenase** on, altered arabitol metabolism and xylitol manufacture in relation to)
- IT Candida diddensii  
Dendryphiella salina  
Fungi  
Pichia farinosa  
**Saccharomyces rouxii**  
Schizophyllum commune  
Torulaspora hansenii  
Torulopsis candida  
**Yeast**  
(xylitol manufacture with, with altered arabitol metabolism)
- IT Fermentation  
(xylitol, with transgenic fungi with altered arabitol metabolism)
- IT Klebsiella terrigena  
(D-arabitol dehydrogenase **gene** of, cloning and expression of, xylitol manufacture in fungi with altered arabitol metabolism in relation to)
- IT **Gene, microbial**  
RL: BIOL (Biological study)  
(URA3, of Candida polymorpha, cloning of, transformation vectors for C. polymorpha and xylitol manufacture in relation to)
- IT **Gene, microbial**  
RL: BIOL (Biological study)  
(gnd, of Escherichia coli, cloning of, alteration of pentose phosphate pathway in xylitol manufacture in relation to)
- IT **Gene, microbial**  
RL: BIOL (Biological study)  
(zwf, of Saccharomyces cerevisiae, cloning of, alteration of pentose phosphate pathway in xylitol manufacture in relation to)
- IT 87-99-0, Xylitol  
RL: BIOL (Biological study)  
(fermentation of, with transgenic **yeast**, modified arabitol metabolism and pentose phosphate pathway in)
- IT 9001-40-5, D-Glucose-6-phosphate dehydrogenase 9024-20-8,  
D-Ribulose-5-phosphate-3-epimerase 9026-40-8, D-Ribulokinase  
9073-95-4, 6-Phospho-D-gluconate dehydrogenase  
RL: BIOL (Biological study)  
(**gene** for, expression of, in fungal hosts with altered arabitol metabolism for manufacture of xylitol)
- IT **9028-16-4, Xylitol dehydrogenase** 9028-18-6,  
D-Arabitol dehydrogenase  
RL: BIOL (Biological study)  
(**gene** for, expression of, in transgenic **yeast**, alteration of arabitol metabolism in xylitol manufacture in relation to)
- IT 9014-48-6, Transketolase **9030-58-4, D-Xylulokinase**  
RL: BIOL (Biological study)  
(**gene** for, inactivation of, in fungal hosts with altered arabitol metabolism for manufacture of xylitol)
- IT 2152-56-9, Arabitol  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(metabolism of, alteration of, in manufacture of xylitol with transgenic

yeasts)

L49 ANSWER 15 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1993:510092 HCAPLUS  
 DN 119:110092  
 ED Entered STN: 18 Sep 1993  
 TI Cloning and improving the expression of *Pichia stipitis* **xylose reductase gene** in *Saccharomyces cerevisiae*  
 AU **Chen, Zhengdao; Ho, Nancy W. Y.**  
 CS Lab. Renewable Resourc. Eng., Purdue Univ., West Lafayette, IN, 47907-1295, USA  
 SO Applied Biochemistry and Biotechnology (1993), 39-40, 135-47  
 CODEN: ABIBDL; ISSN: 0273-2289  
 DT Journal  
 LA English  
 CC 3-2 (Biochemical Genetics)  
 Section cross-reference(s): 16  
 AB The intact *Pichia stipitis* **xylose reductase gene** (XR) has been cloned and expressed in *Saccharomyces cerevisiae*. The possible further improvement of the expression of the *Pichia* **gene** in the new host was studied. To improve the expression of the XR **gene** in **yeast** (*Saccharomyces cerevisiae*), its 5'-noncoding sequence containing the genetic elements for transcription and translation was systematically replaced by that from the **yeast genes**. It was found that the *Pichia* genetic signal for transcription of XR is more effective than the **yeast** TRP5 promoter, but is about half as effective as the **yeast** strong promoter of the alc. dehydrogenase **gene** (ADC1). However, the nucleotide sequence immediately adjacent to the initiation codon of XR, which controls the translation of the **gene** product, seemed to be five times less effective than the corresponding sequence of the ADC1 **gene**. By totally replacing its 5'-noncoding sequence with that of the **yeast** ADC1 **gene**, the expression of XR in **yeast** was nearly ten times higher. Furthermore, the cloned *Pichia* XR described in this article contains very little of its 3'-noncoding sequence. In order to study whether the 3'-noncoding sequence is important to its expression in *S. cerevisiae*, the intact 3'-noncoding sequences of the **yeast xylulokinase gene** was spliced to the 3' end of the PADCl-XR structural **gene**. This latter modification has resulted in a 2-fold further increase in the expression of the *Pichia* XR in **yeast**.  
 ST *Pichia* **xylose reductase gene** cloning  
*Saccharomyces*  
 IT *Saccharomyces cerevisiae*  
 (cloning and expression in, of **xylose reductase gene** of *Pichia stipitis*)  
 IT **Gene**, microbial  
 RL: BIOL (Biological study)  
 (for **xylose reductase**, of *Pichia stipitis*, cloning and expression in *Saccharomyces cerevisiae* of)  
 IT Molecular cloning  
 (of **xylose reductase gene**, of *Pichia stipitis*, in *Saccharomyces cerevisiae*)  
 IT *Pichia stipitis*  
 (**xylose reductase gene** of, cloning and expression of, in *Saccharomyces cerevisiae*)  
 IT 95829-40-6, **Xylose reductase**  
 RL: BIOL (Biological study)  
 (**gene** for, of *Pichia stipitis*, cloning and expression of, in *Saccharomyces cerevisiae*)  
 L49 ANSWER 16 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1993:226769 HCAPLUS



DN 118:226769  
 ED Entered STN: 12 Jun 1993  
 TI Isolation of **xylose reductase gene** of *Pichia stipitis* and its expression in *Saccharomyces cerevisiae*  
 AU Takuma, Shinya; Nakashima, Noriyuki; Tantirungkij, Manee; Kinoshita, Shinichi; Okada, Hirotsuke; Seki, Tatsuji; Yoshida, Toshiomi  
 CS Fac. Eng., Osaka Univ., Suita, 565, Japan  
 SO Applied Biochemistry and Biotechnology (1991), 28-29, 327-40  
 CODEN: ABIBDL; ISSN: 0273-2289  
 DT Journal  
 LA English  
 CC 3-2 (Biochemical Genetics)  
 Section cross-reference(s): 7, 10  
 AB A NADPH/NADH-dependent **xylose reductase gene** was isolated from the xylose-assimilating yeast, *Pichia stipitis*. DNA sequence anal. showed that the **gene** consists of 951 bp. The **gene** introduced in *Saccharomyces cerevisiae* was transcribed to mRNA, and a considerable amount of enzyme activity was observed constitutively, whereas transcription and translation in *P. stipitis* were inducible. *S. cerevisiae* carrying the **xylose reductase gene** could not, however, grow on xylose medium, and could not produce ethanol from xylose. Since xylose uptake and accumulation of xylitol by *S. cerevisiae* were observed, the conversion of xylitol to xylulose seemed to be limited.  
 ST *Pichia xylose reductase gene* cloning  
 sequence; *Saccharomyces* cloning **xylose reductase gene** *Pichia*  
 IT *Saccharomyces cerevisiae*  
 (cloning and expression in, of **xylose reductase gene**, of *Pichia stipitis*)  
 IT **Gene**, microbial  
 RL: BIOL (Biological study)  
 (for **xylose reductase**, of *Pichia stipitis*, cloning and expression and sequencing of)  
 IT Deoxyribonucleic acid sequences  
 (of **xylose reductase gene**, of *Pichia stipitis*)  
 IT Molecular cloning  
 (of **xylose reductase gene**, of *Pichia stipitis*, for expression in yeast)  
 IT Protein sequences  
 (of **xylose reductase**, of *Pichia stipitis*)  
 IT *Pichia stipitis*  
 (**xylose reductase gene** of, sequence and expression in yeast of)  
 IT 138263-97-5  
 RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)  
 (amino acid sequence of, complete)  
 IT 95829-40-6, **Xylose reductase**  
 RL: BIOL (Biological study)  
 (**gene** for, of *Pichia stipitis*, cloning and expression and sequencing of)  
 IT 147651-00-1  
 RL: PRP (Properties); BIOL (Biological study)  
 (nucleotide sequence of)  
 L49 ANSWER 17 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1993:190040 HCAPLUS  
 DN 118:190040  
 ED Entered STN: 14 May 1993  
 TI Secretion of a xylanase from *Cryptococcus albidus* by *Saccharomyces cerevisiae* and *Pichia stipitis*

- AU Morosoli, Rolf; Zalce, Eugenia; Moreau, Alain; Durand, Serge  
 CS Cent. Rech. Microbiol. Appl., Inst. Armand-Frappier, Ville de Laval, QC,  
 H7N 4Z3, Can.  
 SO Progress in Biotechnology (1992), 7(Xylans Xylanases), 247-58  
 CODEN: PBITE3; ISSN: 0921-0423  
 DT Journal  
 LA English  
 CC 16-4 (Fermentation and Bioindustrial Chemistry)  
 Section cross-reference(s): 3  
 AB The xylanase **gene** of *Cryptococcus albidus* and its cDNA were each  
 inserted in the vector pVT100 and in the vector pJHS to transform  
*Saccharomyces cerevisiae* and *Pichia stipitis*, resp. The xylanase  
**gene** was under the control of its own promoter for expts. in *S.*  
*cerevisiae*, while in *P. stipitis* it was under the control of the  
**xylose reductase** promoter of the same strain.  
**Yeasts** transformed with **plasmids** containing the cDNA of the  
 structural xylanase **gene** produced active extracellular xylanase.  
 The enzyme secreted by *S. cerevisiae* had an apparent mol. mass of 48-kDa,  
 which corresponds to that of the native xylanase produced by *C. albidus*.  
 The enzyme synthesized by *P. stipitis*, however, had an apparent mol. mass  
 of 50-kDa, probably reflecting a different protein glycosylation level by  
 this strain. With **plasmids** bearing the genomic xylanase  
**gene**, transcription occurred, but the seven introns interrupting  
 the xylanase **gene** were neither spliced out by *S. cerevisiae* nor  
 by *P. stipitis* and no enzyme was produced. Expression of the xylanase  
**gene** by *P. stipitis*, resulted in a **yeast** able to grow on  
 xylan as carbon source, directly fermenting it to ethanol under anaerobic  
 conditions.  
 ST *Cryptococcus* xylanase **gene** cloning *Saccharomyces Pichia*  
 IT *Pichia stipitis*  
     *Saccharomyces cerevisiae*  
     (cloning and expression in, of xylanase **gene** of *Cryptococcus*  
     *albidus*)  
 IT **Gene**, microbial  
 RL: BIOL (Biological study)  
     (for xylanase, of *Streptococcus albidus*, cloning and expression in  
     *Saccharomyces cerevisiae* and *Pichia stipitis* of)  
 IT Molecular cloning  
     (of xylanase **gene**, of *Cryptococcus albidus*, in *Saccharomyces*  
     *cerevisiae* and *Pichia stipitis*)  
 IT *Cryptococcus albidus*  
     (xylanase **gene** of, cloning and expression of, in  
     *Saccharomyces cerevisiae* and *Pichia stipitis*)  
 IT 37278-89-0, Xylanase  
 RL: BIOL (Biological study)  
     (**gene** for, of *Cryptococcus albidus*, cloning and expression in  
     *Saccharomyces cerevisiae* and *Pichia stipitis* of)
- L49 ANSWER 18 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1993:123016 HCAPLUS  
 DN 118:123016  
 ED Entered STN: 30 Mar 1993  
 TI Xylitol production by recombinant *Saccharomyces cerevisiae*  
 AU Hallborn, Johan; Walfridsson, Mats; Airaksinen, Ulla; Ojamo, Heikki;  
 Hahn-Hagerdal, Barbel; Penttila, Merja; Keranen, Sirkka  
 CS VTT Biotech. Lab., Espoo, SF-02151, Finland  
 SO Bio/Technology (1991), 9(11), 1090-5  
 CODEN: BTCHDA; ISSN: 0733-222X  
 DT Journal  
 LA English  
 CC 16-2 (Fermentation and Bioindustrial Chemistry)  
 Section cross-reference(s): 3, 7, 10  
 AB Efficient conversion of xylose to xylitol was obtained by transforming

Saccharomyces cerevisiae with the **gene** encoding the **xylose reductase** (XR) of Pichia stipitis CBS 6054. Comparison of the **chromosomal** and cDNA copies of the **XYL1 gene** showed that the genomic **XYL1** contains no introns, and an XR monomer of 318 amino acids (35,985 Da) is encoded by an open reading frame of 954 bp. The amino acid sequence of the P. stipitis XR is similar to several **aldose reductases**, suggesting that P. stipitis XR is part of the aldoketo reductase superfamily. S. cerevisiae transformed with the **XYL1 gene** gave over 95% conversion of xylose into xylitol, a yield not obtainable with natural xylose utilizing yeasts.

- ST xylitol ferment xylose recombinant Saccharomyces; **xylose reductase gene** **XYL1** sequence Pichia
- IT **Saccharomyces cerevisiae**  
(cloning and expression in, of **xylose reductase gene** of Pichia stipitis)
- IT Molecular cloning  
(of **xylose reductase gene**, of Pichia stipitis, in Saccharomyces cerevisiae)
- IT Protein sequences  
(of **xylose reductase**, of Pichia stipitis)
- IT Fermentation  
(xylitol, from xylose by recombinant Saccharomyces cerevisiae)
- IT Pichia stipitis  
(**xylose reductase** of, **gene** for, cloning and sequence of)
- IT Deoxyribonucleic acid sequences  
(complementary, for **xylose reductase** of Pichia stipitis)
- IT **Gene**, microbial  
RL: BIOL (Biological study)  
(**XYL1**, for **xylose reductase**, of Pichia stipitis, cloning and sequence of)
- IT **138263-97-5, Xylose reductase** (Pichia stipitis reduced)  
RL: PRP (Properties); BIOL (Biological study)  
(amino acid sequence of, complete)
- IT **95829-40-6, Xylose reductase**  
RL: BIOL (Biological study)  
(**gene** for, of Pichia stipitis, cloning and sequence of)
- IT **87-99-0P, Xylitol**  
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP (Preparation)  
(manufacture of, from xylose by recombinant Saccharomyces cerevisiae)
- IT **146409-21-4**  
RL: PRP (Properties)  
(nucleotide sequence of)
- IT **146409-22-5**  
RL: PRP (Properties)  
(nucleotide sequence of, complete)
- IT **58-86-6, D-Xylose**, uses  
RL: USES (Uses)  
(xylitol manufacture from, by recombinant Saccharomyces cerevisiae)

L49 ANSWER 19 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1993:100558 HCAPLUS  
 DN 118:100558  
 ED Entered STN: 19 Mar 1993  
 TI Xylitol manufacture with **yeast** mutants  
 IN Apajalahti, Juha; Leisola, Matti  
 PA Xyrofin Oy, Finland  
 SO PCT Int. Appl., 33 pp.  
 CODEN: PIXXD2

DT Patent  
 LA English  
 IC ICM C12P007-18  
 CC 16-5 (Fermentation and Bioindustrial Chemistry)  
 Section cross-reference(s): 10

FAN.CNT 1

|      | PATENT NO.  | KIND | DATE     | APPLICATION NO. | DATE         |
|------|---|------|----------|-----------------|--------------|
| PI   | WO 9301299  | A1   | 19930121 | WO 1992-FI203   | 19920630 <-- |
|      | W: CA, DE, FI, GB, JP, NL, NO   |      |          |                 |              |
|      | RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, MC, NL, SE  |      |          |                 |              |
|      | CA 2112374  | AA   | 19930121 | CA 1992-2112374 | 19920630 <-- |
|      | CA 2112374  | C    | 20021029 |                 |              |
|      | EP 604429   | A1   | 19940706 | EP 1992-912764  | 19920630 <-- |
|      | EP 604429   | B1   | 19991020 |                 |              |
|      | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, MC, NL, SE   |      |          |                 |              |
|      | JP 07500492   | T2   | 19950119 | JP 1993-501989  | 19920630 <-- |
|      | JP 3331343  | B2   | 20021007 |                 |              |
|      | AT 185841   | E    | 19991115 | AT 1992-912764  | 19920630 <-- |
|      | ES 2140411  | T3   | 20000301 | ES 1992-912764  | 19920630 <-- |
|      | FR 2678637  | A1   | 19930108 | FR 1992-8109    | 19920701 <-- |
|      | FR 2678637  | B1   | 19960209 |                 |              |
|      | US 6271007  | B1   | 20010807 | US 1994-194624  | 19940207 <-- |
| PRAI | FI 1991-3197  | A    | 19910701 | <--             |              |
|      | US 1992-905870  | B1   | 19920630 | <--             |              |
|      | WO 1992-FI203   | W    | 19920630 | <--             |              |
| AB   | Xylitol is manufactured with <b>yeast</b> mutants defective in xylose metabolism<br>Kluyveromyces marxianus was mutagenized with acriflavine or ethylmethane<br>sulfonate the treated with benomyl. Strains unable to metabolize xylose<br>effectively were selected on xylose- and nystatin-containing medium. Xylitol<br>production rates of 2.8 g/L/h were achieved with one mutant. |      |          |                 |              |
| ST   | xylitol manuf <b>yeast</b> mutant   |      |          |                 |              |
| IT   | Candida<br>Candida utilis<br>Hansenula<br>Kluyveromyces<br>Kluyveromyces marxianus<br>Kluyveromyces marxianus bulgaricus<br>Kluyveromyces marxianus lactis<br>Kluyveromyces marxianus marxianus<br>Pichia<br>(xylose metabolism mutants of, for xylitol manufacture)  |      |          |                 |              |
| IT   | Ribozymes<br>RL: BIOL (Biological study)<br>( <b>yeast</b> transformant containing, directed against xylose metabolism,<br>xylitol manufacture with)  |      |          |                 |              |
| IT   | Ribonucleic acids<br>RL: BIOL (Biological study)<br>(antisense, <b>yeast</b> transformant containing, directed against<br>xylose metabolism, xylitol manufacture with)  |      |          |                 |              |
| IT   | <b>9028-16-4, Xylitol dehydrogenase</b><br><b>9030-58-4</b><br>RL: BIOL (Biological study)<br>(inactivating mutation in <b>gene</b> for, <b>yeast</b> for<br>xylitol manufacture containing)  |      |          |                 |              |
| IT   | 87-99-0P, Xylitol<br>RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP<br>(Preparation)<br>(manufacture of, <b>yeast</b> mutants for)  |      |          |                 |              |
| IT   | 58-86-6, Xylose, uses<br>RL: BIOL (Biological study)<br>( <b>yeast</b> deficient in metabolism of, in preparation of, xylitol manufacture<br>in relation to)  |      |          |                 |              |

L49 ANSWER 20 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1993:96990 HCAPLUS  
 DN 118:96990  
 ED Entered STN: 19 Mar 1993  
 TI Cloning and expression in *Saccharomyces cerevisiae* of the  
 NAD(P)H-dependent **xylose reductase**-encoding  
**gene** (XYL1) from the xylose-assimilating yeast *Pichia*  
*stipitis*  
 AU Amore, Rene; Koetter, Peter; Kuester, Christina; Ciriacy, Michael;  
 Hollenberg, Cornelis P.  
 CS Inst. Mikrobiol., Heinrich-Heine-Univ., Duesseldorf, 4000, Germany  
 SO Gene (1991), 109(1), 89-97  
 CODEN: GENED6; ISSN: 0378-1119  
 DT Journal  
 LA English  
 CC 7-5 (Enzymes)  
 Section cross-reference(s): 3  
 AB The XYL1 **gene** of the yeast *P. stipitis* was isolated  
 from a genomic library using a specific cDNA probe, and its nucleotide  
 (nt) sequence was determined. In the 5' noncoding region of the *P. stipitis*  
 XYL1 **gene**, a TATAAA element (known to be necessary for  
 transcription initiation in most **yeast genes**) is found  
 at nt -81, and two CCAAT recognition motifs (often referred to as the  
 CCAAT box) are present at nt -146 and -106. The XYL1 encodes a  
 polypeptide of 35,927 Da that constitutes a NADH/NADPH-dependent  
**xylose reductase** (XR). The enzyme is part of the  
 xylose-xylulose pathway that is absent or only weakly expressed in *S.*  
*cerevisiae*. Extensive homol. is found to the N terminus of the XR of  
*Pachysolen tannophilus* and *Candida shehatae*. None of the known cofactor  
 binding domains found in many NAD-dependent dehydrogenases are present in  
 the protein. Transformants of *S. cerevisiae* containing XYL1 of *P. stipitis*  
 synthesize an active XR. Fusion of XYL1 with the prokaryotic *tac* promoter  
 leads to a **gene** that can be expressed in *S. cerevisiae* and  
*Escherichia coli*.  
 ST **xylose reductase gene** *Pichia* sequence  
 cloning  
 IT *Pichia stipitis*  
 (NADH/NADPH-dependent **xylose reductase gene**  
 of, cloning and sequence and expression of)  
 IT *Escherichia coli*  
**Saccharomyces cerevisiae**  
 (cloning in, of XYL1 **gene** of *Pichia stipitis*)  
 IT Deoxyribonucleic acid sequences  
 (for NADH/NADPH-dependent **xylose reductase**  
**gene**, of *Pichia stipitis*)  
 IT Protein sequences  
 (for NADH/NADPH-dependent **xylose reductase**, of  
*Pichia stipitis*)  
 IT Molecular cloning  
 (of XYL1 **gene** of *Pichia stipitis*, in *Escherichia coli* and  
*Saccharomyces cerevisiae*)  
 IT **Gene**, microbial  
 RL: BIOL (Biological study)  
 (XYL1, of *Pichia stipitis*, cloning and sequence and expression of)  
 IT 138263-97-5, NADH/NADPH-dependent **xylose**  
**reductase** (*Pichia stipitis*  $\lambda$ gt11 clone reduced)  
 RL: PRP (Properties); BIOL (Biological study)  
 (amino acid sequence of, complete)  
 IT 95829-40-6  
 RL: BIOL (Biological study)  
 (**gene** for, of *Pichia stipitis*, cloning and sequence and  
 expression of)

IT 138575-99-2, **DNA** (*Pichia stipitis*  $\lambda$ gt11 clone XYL1 **gene** and flanking region)  
 RL: PRP (Properties); BIOL (Biological study)  
 (nucleotide sequence of)

IT 138575-98-1  
 RL: PRP (Properties); BIOL (Biological study)  
 (nucleotide sequence of, complete)

L49 ANSWER 21 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1992:52957 HCAPLUS  
 DN 116:52957  
 ED Entered STN: 21 Feb 1992  
 TI Cloning of **yeast xylose reductase** and **xylitol dehydrogenase genes** and their use  
 IN Strasser, Alexander W. M.; Hollenberg, Cornelis P.; Von Ciriacy-Wantrup, Michael; Koetter, Peter; Amore, Rene; Piontek, Michael; Hagedorn, Jutta  
 PA Rhein Biotech Gesellschaft fuer neue Biotechnologische Prozesse und Produkte m.b.H., Germany  
 SO Ger. Offen., 51 pp.  
 CODEN: GWXXBX  
 DT Patent  
 LA German  
 IC ICM C12N001-19  
 ICS C12N015-63; C12P019-34; C07H021-04; C07K015-04  
 CC 3-4 (Biochemical **Genetics**)  
 FAN.CNT 1

|      | PATENT NO.   | KIND | DATE     | APPLICATION NO. | DATE         |
|------|--|------|----------|-----------------|--------------|
| PI   | DE 4009676   | A1   | 19911002 | DE 1990-4009676 | 19900326 <-- |
|      | DE 4009676   | C2   | 19930909 |                 |              |
|      | EP 450430  | A2   | 19911009 | EP 1991-104558  | 19910322 <-- |
|      | EP 450430  | A3   | 19920102 |                 |              |
|      | EP 450430  | B1   | 19970625 |                 |              |
|      | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE  |      |          |                 |              |
|      | AT 154829  | E    | 19970715 | AT 1991-104558  | 19910322 <-- |
|      | ES 2104626   | T3   | 19971016 | ES 1991-104558  | 19910322 <-- |
|      | CA 2039021   | AA   | 19910927 | CA 1991-2039021 | 19910325 <-- |
|      | JP 06339383  | A2   | 19941213 | JP 1991-62160   | 19910326 <-- |
|      | JP 3122153   | B2   | 20010109 |                 |              |
|      | JP 2000139486  | A2   | 20000523 | JP 2000-589     | 19910326 <-- |
|      | JP 2001103988  | A2   | 20010417 | JP 2000-276227  | 19910326 <-- |
|      | JP 3193917   | B2   | 20010730 |                 |              |
| PRAI | DE 1990-4009676  | A    | 19900326 | <--             |              |
|      | JP 1991-62160  | A3   | 19910326 | <--             |              |
| AB   | The XYL1 <b>gene</b> encoding <b>xylose reductase</b> and the XYL2 <b>gene</b> encoding <b>xylitol dehydrogenase</b> of <i>Pichia stipitis</i> are cloned, sequenced, and expressed in other microorganisms. <b>Yeast</b> transformants expressing these <b>genes</b> can be used to prepare EtOH, alc. beverages, or biomass. The promoters of these <b>genes</b> can be used to express <b>genes</b> in <b>yeast</b> . A <i>Saccharomyces cerevisiae</i> mutant containing both <b>genes</b> was prepared and used to prepare EtOH in .apprx.80% yield from xylose. <b>Plasmids</b> containing <i>Clostridium thermocellum</i> cellulase <b>gene</b> linked to the promoter of XYL1 or XYL2 were prepared and <i>P. stipitis</i> transformed with them. These transformants produced the enzyme in response to xylose induction. |      |          |                 |              |
| ST   | XYL1 XYL2 <b>gene</b> <i>Pichia</i> cloning; <b>xylose reductase gene</b> <i>Pichia</i> ; <b>xylitol dehydrogenase gene</b> <i>Pichia</i> ; <i>Saccharomyces</i> transformant ethanol manuf xylose   |      |          |                 |              |
| IT   | Fermentation<br>(alc., <b>yeast</b> expressing XYL1 and/or XYL2 <b>genes</b> of <i>Pichia stipitis</i> for)  |      |          |                 |              |

- IT Paecilomyces
  - Saccharomyces cerevisiae**
  - Schizosaccharomyces
  - Schizosaccharomyces pombe
  - Zymomonas
    - (expression in, of XYL1 and XYL2 **genes** of Pichia stipitis)
- IT Protein sequences
  - (of **xylitol dehydrogenase** of Pichia stipitis, complete)
- IT Protein sequences
  - (of **xylose reductase** of Pichia stipitis, complete)
- IT Molecular cloning
  - (of XYL1 and XYL2 **genes** of Pichia stipitis, in yeast )
- IT **Plasmid** and Episome
  - (pMPGC1-2, cellulase **gene** of Clostridium on, expression in Pichia stipitis of)
- IT **Plasmid** and Episome
  - (pR2, **xylose reductase gene** XYL1 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
- IT **Plasmid** and Episome
  - (pXDH, **xylitol dehydrogenase gene** XYL2 fragment of Pichia stipitis on)
- IT **Plasmid** and Episome
  - (pXDH-HIS3, **xylitol dehydrogenase gene** XYL2 of Pichia stipitis on, expression in Schizosaccharomyces pombe of)
- IT **Plasmid** and Episome
  - (pXR, **xylose reductase gene** XYL1 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
- IT **Plasmid** and Episome
  - (pXR-LEU2, **xylose reductase gene** XYL1 of Pichia stipitis on, expression in Schizosaccharomyces pombe of)
- IT **Plasmid** and Episome
  - (pXRa, **xylose reductase gene**, XYL1 fragment of Pichia stipitis on)
- IT **Plasmid** and Episome
  - (pXRb, **xylose reductase gene** XYL1 fragment of Pichia stipitis on)
- IT Biomass
  - (preparation of, **yeast** expressing XYL1 and/or XYL2 **genes** of Pichia stipitis for)
- IT Deoxyribonucleic acid sequences
  - (**xylitol dehydrogenase**-specifying, of Pichia stipitis, complete)
- IT Candida
  - Debaryomyces
  - Hansenula
  - Kluyveromyces
  - Metschnikowia
  - Pachysolen (fungus)
  - Pichia
    - Saccharomyces**
    - Schwanniomyces
      - (**xylose reductase** and **xylitol dehydrogenase genes** of, cloning of, cloning of XYL1 and XYL2 **genes** of Pichia stipitis in relation to)
- IT Deoxyribonucleic acid sequences
  - (**xylose reductase**-specifying, of Pichia stipitis, complete)
- IT Pichia stipitis
  - (XYL1 and XYL2 **genes** of, cloning and expression in **yeast** of)
- IT **Plasmid** and Episome

- (pD1, **xylitol dehydrogenase gene** XYL2 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
- IT **Plasmid and Episome**  
(pD2, **xylitol dehydrogenase gene** XYL2 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
- IT **Plasmid and Episome**  
(pR1, **xylose reductase gene** XYL1 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
- IT **Plasmid and Episome**  
(pRD1, **xylose reductase gene** XYL1 and **xylitol dehydrogenase gene** XYL2 of Pichia stipitis on, expression in Saccharomyces cerevisiae of)
- IT **Genetic element**  
RL: BIOL (Biological study)  
(promoter, of XYL1 and XYL2 **genes** of Pichia stipitis, heterologous **gene** expression in **yeast** using)
- IT **Gene, microbial**  
RL: BIOL (Biological study)  
(XYL1, cloning and expression of, of Pichia stipitis, in **yeast**)
- IT **Gene, microbial**  
RL: BIOL (Biological study)  
(XYL2, cloning and expression of, of Pichia stipitis, in **yeast**)
- IT 136511-83-6 **138263-97-5**  
RL: BIOL (Biological study)  
(amino acid sequence of and expression in Saccharomyces of **gene** for)
- IT 136510-54-8, Deoxyribonucleic acid (Pichia stipitis clone pD1 **gene** XYL2) 136510-55-9, Deoxyribonucleic acid (Pichia stipitis clone pD1 **gene** XYL2 plus 5'- and 3'-flanking region fragment) 138575-98-1, Deoxyribonucleic acid (Pichia stipitis clone pR1 **gene** XYL1) 138575-99-2, Deoxyribonucleic acid (Pichia stipitis clone pR1 **gene** XYL1 plus 5'- and 3'-flanking region fragment)  
RL: BIOL (Biological study)  
(cloning and expression in Saccharomyces and nucleotide sequence of)
- IT 138575-97-0, Deoxyribonucleic acid (Pichia stipitis clone pD1 **gene** XYL2 promoter region-containing fragment) 138576-00-8, Deoxyribonucleic acid (Pichia stipitis clone pR1 **gene** XYL1 promoter region-containing fragment)  
RL: PRP (Properties)  
(**gene** expression in **yeast** using and nucleotide sequence of)
- IT **9028-16-4, Xylitol dehydrogenase**  
**95829-40-6, Xylose reductase**  
RL: BIOL (Biological study)  
(**gene** for, of Pichia stipitis, cloning and expression in **yeast** of)
- IT 64-17-5P, Ethanol, preparation  
RL: PREP (Preparation)  
(manufacture of, **yeast** transformants expressing XYL1 and XYL2 **genes** of Pichia stipitis for)
- IT 53-57-6P, NADPH 53-59-8P, NADP+  
RL: PREP (Preparation)  
(preparation of, from NADPH, **xylose reductase** of Pichia stipitis for)
- IT 551-84-8, Xylulose  
RL: BIOL (Biological study)  
(**yeast** mutants growing on, XYL1 and XYL2 **genes** of Pichia stipitis expression in and enzyme manufacture with)
- IT 58-86-6, Xylose, biological studies  
RL: BIOL (Biological study)  
(**yeast** transformed with XYL1 and/or XYL2 **genes** of



Pichia growth on, for biomass preparation)

L49 ANSWER 22 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 1992:35663 HCAPLUS

DN 116:35663

ED Entered STN: 08 Feb 1992

TI Recombinant **yeasts** containing DNA sequences coding for  
**xylose reductase** and **xylitol**  
**dehydrogenase**

IN Hallborn, Johan; Penttila, Merja; Ojamo, Heikki; Walfridsson, Mats;  
Airaksinen, Ulla; Keranen, Sirkka; Hahn-Hagerdal, Barbel

PA Valtion Teknillinen Tutkimuskeskus, Finland

SO PCT Int. Appl., 47 pp.

CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-53

ICS C12N009-04

CC 3-4 (Biochemical Genetics)

FAN.CNT 1

|      | PATENT NO.  | KIND | DATE     | APPLICATION NO. | DATE         |
|------|---|------|----------|-----------------|--------------|
| PI   | WO 9115588  | A1   | 19911017 | WO 1991-FI103   | 19910408 <-- |
|      | W: AU, CA, FI, JP, NO, US   |      |          |                 |              |
|      | RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LU, NL, SE  |      |          |                 |              |
|      | FI 9001771  | A    | 19911007 | FI 1990-1771    | 19900406 <-- |
|      | CA 2090122  | AA   | 19911007 | CA 1991-2090122 | 19910408 <-- |
|      | CA 2090122  | C    | 20020618 |                 |              |
|      | AU 9175657  | A1   | 19911030 | AU 1991-75657   | 19910408 <-- |
|      | AU 647104   | B2   | 19940317 |                 |              |
|      | EP 527758   | A1   | 19930224 | EP 1991-906996  | 19910408 <-- |
|      | EP 527758   | B1   | 19980107 |                 |              |
|      | R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE   |      |          |                 |              |
|      | JP 05507843   | T2   | 19931111 | JP 1991-506907  | 19910408 <-- |
|      | JP 3348215  | B2   | 20021120 |                 |              |
|      | AT 161886   | E    | 19980115 | AT 1991-906996  | 19910408 <-- |
|      | ES 2113373  | T3   | 19980501 | ES 1991-906996  | 19910408 <-- |
|      | NO 9203880  | A    | 19921006 | NO 1992-3880    | 19921006 <-- |
|      | US 5866382  | A    | 19990202 | US 1994-336198  | 19941103 <-- |
|      | US 6582944  | B1   | 20030624 | US 1999-184965  | 19990108 <-- |
|      | FI 9902153  | A    | 19991006 | FI 1999-2153    | 19991006 <-- |
| PRAI | FI 1990-1771  | A    | 19900406 |                 | <--          |
|      | US 1990-527775  | A2   | 19900524 |                 | <--          |
|      | WO 1991-FI103   | A    | 19910408 |                 | <--          |
|      | US 1992-848694  | B1   | 19920309 |                 | <--          |
|      | FI 1992-4461  | A    | 19921002 |                 | <--          |
|      | US 1994-336198  | A3   | 19941103 |                 | <--          |
| AB   | A cDNA for <b>yeast xylose reductase</b> is cloned<br>and sequenced. This cDNA is expressed in recombinant <b>yeast</b> ,<br>optionally along with that for <b>xylitol dehydrogenase</b> .<br>These recombinant <b>yeast</b> can be used to prepare xylitol, or ethanol<br>(when both <b>genes</b> are expressed), from xylose or xylose-containing<br>materials. The <b>xylose reductase</b> cDNA of <i>Pichia</i><br><i>stipitis</i> was cloned. <i>Saccharomyces cerevisiae</i> transformants expressing<br>this cDNA were used to prepare xylitol. <i>S. cerevisiae</i> expressing both<br><b>xylose reductase</b> and <b>xylitol</b><br><b>dehydrogenase</b> produced EtOH, xylitol, and biomass from spent<br>sulfite liquor. |      |          |                 |              |
| ST   | <b>xylose reductase</b> cDNA <i>Pichia</i> cloning; xylitol ethanol<br>manuf recombinant <i>Saccharomyces</i>   |      |          |                 |              |
| IT   | <b>Gene</b> , microbial   |      |          |                 |              |
|      | RL: BIOL (Biological study)   |      |          |                 |              |
|      | (cDNA, for <b>xylose reductase</b> of <i>Pichia stipitis</i> ,  |      |          |                 |              |

- cloning and expression in *Saccharomyces cerevisiae* of)
- IT Kluyveromyces  
Pichia  
**Saccharomyces cerevisiae**  
Schizosaccharomyces pombe  
Yeast  
(expression in, of **xylose reductase** cDNA of *Pichia stipitis*)
- IT Molecular cloning  
(of **xylose reductase** cDNA of *Pichia stipitis*, in *Saccharomyces cerevisiae*)
- IT Protein sequences  
(of **xylose reductase** of *Pichia stipitis*, complete)
- IT Plasmid and Episome  
(pJHXDH60, **xylitol dehydrogenase** cDNA of *Pichia stipitis* on, expression in *Saccharomyces cerevisiae* of)
- IT Plasmid and Episome  
(pJHXDH70, **xylitol dehydrogenase** cDNA of *Pichia stipitis* on, expression in *Saccharomyces cerevisiae* of)
- IT Plasmid and Episome  
(pJHXR22, **xylose reductase** cDNA of *Pichia stipitis* on, expression in *Saccharomyces cerevisiae* of)
- IT Plasmid and Episome  
(pMW22, **xylitol dehydrogenase** cDNA of *Pichia stipitis* on, expression in *Saccharomyces cerevisiae* of)
- IT Plasmid and Episome  
(pUA103, **xylose reductase** cDNA of *Pichia stipitis* on, expression in *Saccharomyces cerevisiae* of)
- IT Plasmid and Episome  
(pUA107, **xylose reductase** cDNA of *Pichia stipitis* on, expression in *Saccharomyces cerevisiae* of)
- IT *Pichia stipitis*  
(**xylose reductase** cDNA of, cloning and expression in *Saccharomyces cerevisiae* of)
- IT Deoxyribonucleic acid sequences  
(**xylose reductase**-specifying, of *Pichia stipitis*, complete)
- IT 138263-97-5  
RL: PRP (Properties); BIOL (Biological study)  
(amino acid sequence of and cloning of cDNA for)
- IT 95829-40-6, **Xylose reductase**  
RL: BIOL (Biological study)  
(cDNA for, of *Pichia stipitis*, cloning and expression in *Saccharomyces cerevisiae* of)
- IT 9028-16-4, **Xylitol dehydrogenase**  
RL: BIOL (Biological study)  
(cDNA for, recombinant **yeast** expressing **xylose reductase** cDNA and, ethanol manufacture with)
- IT 138263-60-2, Deoxyribonucleic acid (*Pichia stipitis* clone pUA103 **gene** xrd minus terminator fragment)  
RL: PRP (Properties); BIOL (Biological study)  
(cloning and nucleotide sequence of)
- IT 87-99-0P, Xylitol  
RL: PREP (Preparation)  
(manufacture of, from xylose, recombinant **yeast xylose reductase** for)
- IT 64-17-5P, Ethanol, preparation  
RL: PREP (Preparation)  
(manufacture of, recombinant **yeast** expressing **xylose reductase** and **xylitol dehydrogenase** cDNAs for)
- IT 58-86-6, Xylose, biological studies  
RL: BIOL (Biological study)

(xylitol manufacture from, recombinant **yeast** expressing cloned  
**xylose reductase** cDNA for)

L49 ANSWER 23 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1991:576285 HCAPLUS  
 DN 115:176285  
 ED Entered STN: 01 Nov 1991  
 TI Isolation and characterization of the *Pichia stipitis* **xylitol dehydrogenase gene**, XYL2, and construction of a xylose-utilizing *Saccharomyces cerevisiae* transformant  
 AU Koetter, Peter; Amore, Rene; Hollenberg, Cornelis P.; Ciriacy, Michael  
 CS Inst. Mikrobiol., Heinrich-Heine-Univ., Duesseldorf, W-4000, Germany  
 SO Current Genetics (1990), 18(6), 493-500  
 CODEN: CUGED5; ISSN: 0172-8083  
 DT Journal  
 LA English  
 CC 3-3 (Biochemical Genetics)  
 AB A *P. stipitis* cDNA library in  $\lambda$ gt11 was screened using antisera against *P. stipitis* **xylose reductase** and **xylitol dehydrogenase**, resp. The resulting cDNA clones served as probes for screening a *P. stipitis* genomic library. The genomic XYL2 **gene** was isolated and the nucleotide sequence of the 1089-bp structural **gene**, and of adjacent non-coding regions, was determined. The XYL2 open-reading frame codes for a protein of 363 amino acids with a predicted mol. mass of 38.5 kDA. The XYL2 **gene** is actively expressed in *S. cerevisiae* transformants. *S. cerevisiae* cells transformed with a **plasmid**, pRD1, containing both the **xylose reductase gene** (XYL1) and the **xylitol dehydrogenase gene** (XYL2), were able to grow on xylose as a sole carbon source. In contrast to aerobic glucose metabolism, *S. cerevisiae* XYL1-XYL2 transformants utilize xylose almost entirely oxidatively.

ST *Pichia* **xylitol dehydrogenase gene** XYL2  
 sequence; transformation *Saccharomyces* **xylitol dehydrogenase gene** *Pichia*

IT *Saccharomyces cerevisiae*  
 (cloning and expression in, of **xylitol dehydrogenase** and **xylose reductase genes** of *Pichia stipitis*)

IT Protein sequences  
 (of **xylitol dehydrogenase**, of *Pichia stipitis*, complete)

IT Transformation, genetic  
 (of *Saccharomyces cerevisiae*, with *Pichia stipitis* xylose metabolism **genes** XYL1 and XYL2)

IT Codon  
 RL: BIOL (Biological study)  
 (usage of, in **xylitol dehydrogenase gene** XYL2, of *Pichia stipitis*)

IT *Pichia stipitis*  
 (**xylitol dehydrogenase gene** XYL2 of, structure and cloning and expression in *Saccharomyces cerevisiae* of)

IT Deoxyribonucleic acid sequences  
 (**xylitol dehydrogenase**-specifying, of *Pichia stipitis*, complete)

IT **Plasmid** and Episome  
 (pRD1, cloning vector for **xylitol dehydrogenase** and **xylose reductase genes**, expression in *Saccharomyces cerevisiae* of)

IT **Gene** and Genetic element, microbial  
 RL: BIOL (Biological study)  
 (XYL1, for **xylose reductase**, of *Pichia stipitis*, cloning and expression in *Saccharomyces cerevisiae* of)

- IT **Gene** and Genetic element, microbial  
RL: BIOL (Biological study)  
(XYL2, for **xylitol dehydrogenase**, of *Pichia stipitis*, structure and cloning and expression in *Saccharomyces cerevisiae* of)
- IT 136511-83-6  
RL: PRP (Properties)  
(amino acid sequence of)
- IT **95829-40-6, Xylose reductase**  
RL: PRP (Properties)  
(**gene** for, of *Pichia stipitis*, cloning and expression in *Saccharomyces cerevisiae* of)
- IT **9028-16-4, Xylitol dehydrogenase**  
RL: PRP (Properties)  
(**gene** for, of *Pichia stipitis*, sequence and expression in *Saccharomyces cerevisiae* of)
- IT 58-86-6, Xylose, biological studies  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)  
(metabolism of, by *Saccharomyces cerevisiae* transformant containing *Pichia stipitis* **genes** XYL1 and XYL2)
- IT 136510-55-9, Deoxyribonucleic acid (*Pichia stipitis* clone pD1 **gene** XYL2 plus 5'- and 3'-flanking region fragment)  
RL: PRP (Properties)  
(nucleotide sequence in)
- IT 136510-54-8, Deoxyribonucleic acid (*Pichia stipitis* clone pD1 **gene** XYL2)  
RL: PRP (Properties); BIOL (Biological study)  
(nucleotide sequence of)
- L49 ANSWER 24 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1990:492753 HCAPLUS  
DN 113:92753  
ED Entered STN: 16 Sep 1990  
TI Isolation of cDNA clones using **yeast** artificial **chromosome** probes  
AU Elvin, P.; Slyn, G.; Black, D.; Graham, A.; Butler, R.; Riley, J.; Anand, R.; Markham, A. F.  
CS Eep. Biotechnol., ICI Pharm., Cheshire, SK10 4TG, UK  
SO Nucleic Acids Research (1990), 18(13), 3913-17  
CODEN: NARHAD; ISSN: 0305-1048  
DT Journal  
LA English  
CC 3-4 (Biochemical **Genetics**)  
AB The cloning of large **DNA** fragments of hundreds of kilobases in **yeast** artificial **chromosomes** has simplified the anal. of regions of the genome previously cloned by cosmid walking. The mapping of expressed sequences within cosmid contigs has relied on the association of **genes** with sequence motifs defined by rare-cutting endonucleases, and the identification of sequence conservation between species. It was reasoned that if the contribution of repetitive sequences to filter hybridizations could be minimized, then the use of large cloned **DNA**s as hybridization probes to screen cDNA libraries would greatly simplify the characterization of hitherto unidentified **genes**. The use of this approach is demonstrated by using a YAC, containing 180kb of human genomic **DNA** including the **aldose reductase gene**, as a probe to isolate an **aldose reductase** cDNA from a  $\lambda$ gt11 human fetal liver cDNA library.
- ST human **aldose reductase** cDNA detection YAC; cDNA detection cosmid YAC **gene** probe; **yeast** artificial **chromosome** probe cDNA identification
- IT **Gene** and Genetic element, animal  
RL: BIOL (Biological study)

- (for **aldose reductase**, of human, **yeast**  
artificial **chromosome** vector for isolation of cDNA for)
- IT **Gene** and Genetic element  
RL: BIOL (Biological study)  
(isolation of, **yeast** artificial **chromosome** containing  
genomic inserts as probes for)
- IT Molecular cloning  
(**yeast** artificial **chromosome** as probe for, cDNA  
library screening with)
- IT **Chromosome**  
(**yeast** artificial, isolation of cDNA clones using  
**chromosomal** probes cloned in)
- IT **9028-31-3**  
RL: PRP (Properties)  
(cDNA library containing sequence for human, homologous **gene** in  
**yeast** artificial **chromosome** as probe for detection  
of)
- L49 ANSWER 25 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1990:422145 HCAPLUS  
DN 113:22145  
ED Entered STN: 21 Jul 1990  
TI **Xylulokinase** activity in various **yeasts** including  
Saccharomyces cerevisiae containing the cloned **xylulokinase**  
**gene**
- AU Deng, Xue Xing; Ho, Nancy W. Y.  
CS A. A. Potter Eng. Cent., Purdue Univ., West Lafayette, IN, 47907, USA  
SO Applied Biochemistry and Biotechnology (1990), 24-25, 193-9  
CODEN: ABIBDL; ISSN: 0273-2289  
DT Journal  
LA English  
CC 16-5 (Fermentation and Bioindustrial Chemistry)  
Section cross-reference(s): 3, 10
- AB D-Xylose is a major constituent of hemicellulose, which makes up 20-30% of  
the renewable biomass in nature. D-Xylose can be fermented by most  
**yeasts**, including S. cerevisiae, by a 2-stage process. In this  
process, xylose is 1st converted to xylulose in vitro by xylose (glucose)  
isomerase, and the latter sugar is then fermented by **yeast** to  
EtOH. With the availability of an inexpensive source of xylose isomerase  
produced by recombinant Escherichia coli, this process of fermenting  
xylose to EtOH can become quite effective. **Yeast** xylose and  
xylulose fermentation was further improved by cloning and overexpression of the  
**xylulokinase gene**. For instance, the level of  
**xylulokinase** activity in S. cerevisiae was increased 230-fold by  
cloning its **xylulokinase gene** on a high copy-number  
**plasmid**, coupled with fusion of the **gene** with an  
effective promoter. The resulting genetically engineered **yeasts**  
can ferment xylose and xylulose more than twice as fast as the parent  
**yeast**.
- ST **xylulokinase gene** cloning **yeast** ethanol  
fermn; Saccharomyces xylulose fermn **xylulokinase gene**
- IT Fermentation  
(ethanol, from xylose by **yeast**, **xylulokinase**  
**gene** cloning in)
- IT **Gene** and Genetic element, microbial  
RL: PROC (Process)  
(for **xylulokinase**, cloning of, in **yeast** for ethanol  
fermentation)
- IT Molecular cloning  
(of **xylulokinase gene**, in **yeast** for  
ethanol fermentation)
- IT **Yeast**  
(**xylulokinase** activities in)

- IT **Saccharomyces cerevisiae**  
(**xylulokinase gene** cloning in, for ethanol fermentation)
- IT 58-86-6, Xylose, biological studies  
RL: BIOL (Biological study)  
(ethanol fermentation of, by **yeast, xylulokinase gene** cloning in)
- IT 9030-58-4, **Xylulokinase**  
RL: BIOL (Biological study)  
(**gene** for, cloning of, in **yeast** for ethanol fermentation)
- IT 64-17-5P, Ethanol, preparation  
RL: BMF (Bioindustrial manufacture); BIOL (Biological study); PREP  
(Preparation)  
(manufacture of, from xylose by **yeast, xylulokinase gene** cloning in)
- L49 ANSWER 26 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1990:94337 HCAPLUS  
DN 112:94337  
ED Entered STN: 18 Mar 1990  
TI Purification, characterization, and amino terminal sequence of  
**xylose reductase** from *Candida shehatae*  
AU Ho, N. W. Y.; Lin, F. P.; Huang, S.; Andrews, P. C.; Tsao, G. T.  
CS Lab. Renewable Resourc. Eng., Purdue Univ., West Lafayette, IN, 47907, USA  
SO Enzyme and Microbial Technology (1990), 12(1), 33-9  
CODEN: EMTED2; ISSN: 0141-0229  
DT Journal  
LA English  
CC 7-2 (Enzymes)  
Section cross-reference(s): 16
- AB A convenient and reliable procedure for the purification of **xylose reductase** from *C. shehatae* to near homogeneity was developed. The amino acid composition and N-terminal sequence of the enzyme were also analyzed. *C. shehatae* seems to contain only 1 **xylose reductase**, but the enzyme has a dual coenzyme specificity for both NADPH and NADH. The enzyme is remarkably stable at room temperature and 4°. Xylose fermentation is by NADH-dependent activity.
- ST **xylose reductase** *Candida*; xylose fermn **xylose reductase** NADH *Candida*
- IT Protein sequences  
(of **xylose reductase** N-terminus, of *Candida shehatae*)
- IT Amino acids, biological studies  
RL: BIOL (Biological study)  
(of **xylose reductase**, of *Candida shehatae*)
- IT Fermentation  
(of xylose, by **xylose reductase** of **yeast**, NADH-dependent activity in)
- IT *Candida shehatae*  
(**xylose reductase** of, purification and N-terminal amino acid sequence and other properties of)
- IT 58-86-6, D-Xylose, biological studies  
RL: BIOL (Biological study)  
(fermentation of, by **yeast xylose reductase**, NADH-dependent activity in)
- IT 95829-40-6P, **Xylose reductase**  
RL: PREP (Preparation)  
(of *Candida shehatae*, purification and N-terminal amino acid sequence and other properties of)
- IT 53-57-6, NADPH  
RL: BIOL (Biological study)  
(**xylose reductase** of *Candida shehatae* requirement for NADH and)
- IT 58-68-4, NADH

RL: BIOL (Biological study)  
(**xylose reductase** of *Candida shehatae* requirement  
for NADPH and)

L49 ANSWER 27 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1989:611729 HCAPLUS  
DN 111:211729  
ED Entered STN: 09 Dec 1989  
TI Metabolism of D-xylose in *Schizosaccharomyces pombe* cloned with a xylose  
isomerase **gene**  
AU Chan, Err Cheng; Ueng, Peter Pear; Chen, Li Fu  
CS Dep. Food Sci., Purdue Univ., West Lafayette, IN, 47907, USA  
SO Applied Microbiology and Biotechnology (1989), 31(5-6), 524-8  
CODEN: AMBIDG; ISSN: 0175-7598  
DT Journal  
LA English  
CC 10-2 (Microbial Biochemistry)  
Section cross-reference(s): 3  
AB The *Escherichia coli* xylose isomerase **gene** was transformed into  
*S. pombe* for direct D-xylose utilization. In order to understand D-xylose  
metabolism and determine the limiting factors on D-xylose utilization by the  
transformed **yeast**, D-xylose transport, xylose isomerization, and  
xylulose phosphorylation were investigated. The results indicated that  
low activity of xylose isomerization in the cloned **yeast** was the  
limiting step for D-xylose fermentation. An in vitro study showed that  
**yeast** proteases decreased xylose isomerase activity. Xylitol, a  
byproduct of D-xylose fermentation, had no effect on the activity of xylose  
isomerase.  
ST xylose metab *Schizosaccharomyces gene* cloning; *Escherichia*  
xylose isomerase **gene** cloning **yeast**  
IT **Gene** and Genetic element, microbial  
RL: BIOL (Biological study)  
(for xylose isomerase, of *Escherichia coli*, xylose metabolism by  
recombinant *Schizosaccharomyces pombe* containing)  
IT Biological transport  
(of xylose, by recombinant xylose isomerase-containing *Schizosaccharomyces*  
*pombe*)  
IT *Schizosaccharomyces pombe*  
(xylose metabolism by recombinant xylose isomerase-containing)  
IT 58-86-6, D-Xylose, biological studies 551-84-8, D-Xylulose  
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL  
(Biological study); PROC (Process)  
(metabolism of, by *Schizosaccharomyces pombe* with xylose isomerase  
**gene**)  
IT 9030-58-4, Xylulokinase  
RL: BIOL (Biological study)  
(of transformed *Schizosaccharomyces pombe* containing xylose isomerase)  
IT 9023-82-9, Xylose isomerase  
RL: BIOL (Biological study)  
(of *Escherichia coli*, xylose metabolism by *Schizosaccharomyces pombe* with)  
  
L49 ANSWER 28 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1989:510301 HCAPLUS  
DN 111:110301  
ED Entered STN: 01 Oct 1989  
TI Construction of **yeast xylulokinase** mutant by  
recombinant **DNA** techniques  
AU Stevis, Panayiotis E.; Ho, Nancy W. Y.  
CS Dep. Foods Nutr., Purdue Univ., West Lafayette, IN, 47907, USA  
SO Applied Biochemistry and Biotechnology (1989), Volume Date 1988,  
20-21, 327-34  
CODEN: ABIBDL; ISSN: 0273-2289  
DT Journal

LA English  
CC 3-5 (Biochemical Genetics)  
AB A *Saccharomyces cerevisiae* **xylulokinase** mutant was constructed by using the cloned **yeast xylulokinase gene**, XYK-Sc, and the **gene** disruption technique. The *S. cerevisiae* LEU2 **gene** was used to disrupt the XYK-Sc **gene** cloned on pLSK4 by insertion into the unique HindIII site of the **gene**. The disrupted **gene** was liberated from the remainder of the **plasmid** with XhoI digestion, yielding a 4.4 kb **DNA** fragment. Transformation of a *S. cerevisiae* leu2 mutant with this fragment and selection for Leu+ complementation resulted in the isolation of transformants that were unable to grow in pure xylulose medium. The ability to grow in xylulose medium and increased **xylulokinase** activity were obtained by transforming the mutant with a **plasmid**-borne wild-type XYK-Sc **gene**. Insertional inactivation of the **chromosomal** XYK-Sc **gene** was also demonstrated by xylulokinase assays.

ST *Saccharomyces xylulokinase gene* mutation recombinant **DNA**  
IT Mutation  
(in **xylulokinase gene**, of *Saccharomyces cerevisiae*, **gene** disruption technique in construction of)  
IT *Saccharomyces cerevisiae* (**xylulokinase gene** of, mutation construction in, by **gene** disruption technique)  
IT **Gene** and Genetic element, microbial  
RL: BIOL (Biological study)  
(XYK, for **xylulokinase**, of *Saccharomyces cerevisiae*, mutation in, **gene** disruption technique for)  
IT 9030-58-4, **Xylulokinase**  
RL: PRP (Properties)  
(**gene** for, of *Saccharomyces cerevisiae*, construction of mutation in, by **gene** disruption technique)

L49 ANSWER 29 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1989:472444 HCAPLUS  
DN 111:72444  
ED Entered STN: 03 Sep 1989  
TI Cloning of **yeast xylulokinase gene** by complementation of *E. coli* and **yeast** mutations  
AU Ho, Nancy W. Y.; Chang, Sue Fen  
CS Lab. Renew. Resour. Eng., Purdue Univ., West Lafayette, IN, USA  
SO Enzyme and Microbial Technology (1989), 11(7), 417-21  
CODEN: EMTED2; ISSN: 0141-0229  
DT Journal  
LA English  
CC 3-4 (Biochemical Genetics)  
AB The **gene** encoding **yeast** (*Saccharomyces cerevisiae*) **xylulokinase** has been isolated by complementation of *Escherichia coli* **xylulokinase** mutations. Through subcloning, the **gene** has been localized on two HindIII fragments (1.2 and 2.4 bp). Within these HindIII fragments, there lies a 2.2-kb XhoI fragment which contains the structural **gene** of **yeast xylulokinase**. Upon insertion of a selectable **gene** into the XhoI fragment, the resulting recombination fragment has been used to construct a **yeast xylulokinase** mutant by the **gene** disruption technique. The cloned **xylulokinase gene** was found to be able to complement such a **xylulokinase** mutant.

ST *Saccharomyces xylulokinase gene* cloning *Escherichia*  
IT **Gene** and Genetic element, microbial  
RL: PROC (Process)  
(for **xylulokinase**, of **yeast**, cloning of)



IT Complementation, genetic  
(of **xylulokinase gene** mutation in *Escherichia coli*,  
by **yeast gene**)

IT Molecular cloning  
(of **xylulokinase gene**, of **yeast**)

IT **Saccharomyces cerevisiae**  
(**xylulokinase gene** of, cloning of)

IT *Escherichia coli*  
(**xylulokinase gene** of, mutation in, **yeast**  
**gene** complementation of)

IT 9030-58-4, **Xylulokinase**  
RL: PRP (Properties)  
(**gene** for, of **yeast**, cloning of)

L49 ANSWER 30 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN

AN 1989:434409 HCAPLUS

DN 111:34409

ED Entered STN: 05 Aug 1989

TI A nuclear **yeast gene** (GCY) encodes a polypeptide with  
high homology to a vertebrate eye lens protein

AU Oechsner, Ulrich; Magdolen, Viktor; Bandlow, Wolfhard

CS Inst. Genet. Microbiol., Munich, D-8000, Fed. Rep. Ger.

SO FEBS Letters (1988), 238(1), 123-8  
CODEN: FEBLAL; ISSN: 0014-5793

DT Journal

LA English

CC 3-3 (Biochemical Genetics)  
Section cross-reference(s): 6

AB The nuclear **gene** for a **yeast** protein is described  
which shows unexpectedly high homol. with mammalian aldo/keto reductases  
as well as with p-crystallin, one of the prominent proteins of the  
frog eye lens. Although it could be proven that the **gene** occurs  
as a single copy in the haploid **yeast** genome, replacement of the  
intact by a disrupted, nonfunctional allele led to no obvious phenotype,  
indicating that the **gene** is dispensable. The **gene** was  
assigned to **chromosome** XV. It is transcribed in vivo into an  
mRNA of about 1300 bases with a coding capacity for a protein of 312 amino  
acids (estimated Mr, 35,000).

ST *Saccharomyces gene* GCY protein sequence

IT **Saccharomyces cerevisiae**  
(**gene** GCY protein of, homol. of, to vertebrate eye lens  
protein)

IT Protein sequences  
(of **gene** GCY protein, of *Saccharomyces cerevisiae*, complete)

IT Eye, composition  
(protein of, of vertebrate, **gene** GCY protein of *Saccharomyces*  
*cerevisiae* homol. with)

IT Proteins, specific or class  
RL: BIOL (Biological study)  
(**gene** GCY, **gene** for, of *Saccharomyces cerevisiae*,  
nucleotide and encoded peptide sequences of)

IT Deoxyribonucleic acid sequences  
(**gene** GCY protein-specifying, of *Saccharomyces cerevisiae*,  
complete)

IT **Gene** and Genetic element, microbial  
RL: BIOL (Biological study)  
(GCY, of *Saccharomyces cerevisiae*, nucleotide and encoded peptide  
sequences of)

IT Crystallins  
RL: BIOL (Biological study)  
(p-, **gene** GCY protein of *Saccharomyces cerevisiae* homol.  
with, of frog)

IT **Chromosome**

- (*Saccharomyces cerevisiae* XV, **gene** GCY localization on)
- IT 121548-71-8, Protein (*Saccharomyces cerevisiae* **gene** GCY reduced)  
 RL: PRP (Properties)  
 (amino acid sequence of)
- IT 121547-66-8, Deoxyribonucleic acid (*Saccharomyces cerevisiae* **gene** GCY)  
 RL: PRP (Properties); BIOL (Biological study)  
 (nucleotide sequence of)
- IT 9028-31-3  
 RL: PRP (Properties)  
 (of eye lens, of rat, **gene** GCY protein of *Saccharomyces cerevisiae* homol. with)
- IT 9028-12-0, Aldehyde reductase  
 RL: PRP (Properties)  
 (of liver of human, **gene** GCY protein of *Saccharomyces cerevisiae* homol. with)
- IT 55976-95-9  
 RL: PRP (Properties)  
 (of lung of cattle, **gene** GCY protein of *Saccharomyces cerevisiae* homol. with)
- L49 ANSWER 31 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
 AN 1989:129846 HCAPLUS  
 DN 110:129846  
 ED Entered STN: 15 Apr 1989  
 TI Cloning the **yeast xylulokinase gene** for the improvement of xylose fermentation  
 AU Chang, Sue Feng; Ho, Nancy W. Y.  
 CS Lab. Renew. Resour. Eng., Purdue Univ., West Lafayette, IN, 47907, USA  
 SO Applied Biochemistry and Biotechnology (1988), 17, 313-18  
 CODEN: ABIBDL; ISSN: 0273-2289  
 DT Journal  
 LA English  
 CC 3-4 (Biochemical Genetics)  
 Section cross-reference(s): 16
- AB **Plasmids** pLSK1 or pLSK3 containing a *Saccharomyces cerevisiae* DNA fragment complemented *Escherichia coli* **xylulokinase** mutations. The cloned **yeast DNA** probably contains all the necessary structural elements of a **yeast gene** encoding a **yeast protein** (enzyme). *E. coli* **xylulokinase** mutants harboring either pLSK1 or pLSK3 synthesized **xylulokinase** in the absence of xylose induction as well as in the presence of glucose (insensitive to glucose inhibition). Thus, the **yeast DNA** fragment cloned on pLSK1 or pLSK3 at least contains the structural **gene** encoding *S. cerevisiae* **xylulokinase**.
- ST **xylulokinase gene** *Saccharomyces* complementation *Escherichia*
- IT *Escherichia coli*  
 (expression in, of **xylulokinase gene** of *Saccharomyces cerevisiae*)
- IT **Gene** and Genetic element, microbial  
 RL: BIOL (Biological study)  
 (for **xylulokinase**, of *Saccharomyces cerevisiae*, structure and expression in *Escherichia coli* of)
- IT Complementation, genetic  
 (of **xylulokinase** mutants of *Escherichia coli*, by *Saccharomyces cerevisiae* **gene**)
- IT **Saccharomyces cerevisiae**  
 (**xylulokinase gene** of, structure and expression in *Escherichia coli* of)
- IT 9030-58-4, **Xylulokinase**  
 RL: PRP (Properties)

(gene for, of yeast, structure and expression in  
Escherichia coli of)

- L49 ANSWER 32 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1988:33023 HCAPLUS  
DN 108:33023  
ED Entered STN: 06 Feb 1988  
TI Cloning of the Pachysolen tannophilus **xylulokinase gene**  
by complementation in Escherichia coli  
AU Stevis, Panayiotis E.; Huang, James J.; Ho, Nancy W. Y.  
CS Lab. Renewable Resour. Eng., Purdue Univ., West Lafayette, IN, 47907, USA  
SO Applied and Environmental Microbiology (1987), 53(12), 2975-7  
CODEN: AEMIDF; ISSN: 0099-2240  
DT Journal  
LA English  
CC 3-4 (Biochemical Genetics)  
AB The **gene** coding for **xylulokinase** has been isolated  
from the **yeast** P. tannophilus by complementation of E. coli  
**xylulokinase** (xylB) mutants. Through subcloning, the **gene**  
has been localized at one end of a 3.2-kilobase EcoRI-PstI fragment.  
Expression of the cloned **gene** was insensitive to glucose  
inhibition. Further, the cloned **gene** did not cross-hybridize  
with E. coli and Saccharomyces cerevisiae **xylulokinase**  
**genes**.  
ST Pachysolen **xylulokinase gene** cloning Escherichia  
IT Escherichia coli  
(cloning in, of **xylulokinase gene** of Pachysolen  
tannophilus)  
IT Molecular cloning  
(of **xylulokinase gene** of Pachysolen tannophilus, in  
Escherichia coli)  
IT Pachysolen tannophilus  
(**xylulokinase gene** of, cloning in Escherichia coli  
of)  
IT **Gene** and Genetic element, microbial  
RL: BIOL (Biological study)  
(XYK, for **xylulokinase**, of Pachysolen tannophilus, cloning in  
Escherichia coli of)  
IT **9030-58-4, Xylulokinase**  
RL: PRP (Properties)  
(**gene** for, of Pachysolen tannophilus, cloning in Escherichia  
coli of)
- L49 ANSWER 33 OF 33 HCAPLUS COPYRIGHT 2004 ACS on STN  
AN 1986:419795 HCAPLUS  
DN 105:19795  
ED Entered STN: 26 Jul 1986  
TI Towards a xylose fermenting **yeast**  
AU Hollenberg, Cornelis P.; Wilhelm, Martin  
CS Inst. Mikrobiol., Univ. Duesseldorf, Duesseldorf, 4000, Fed. Rep. Ger.  
SO Eur. Congr. Biotechnol., 3rd (1984), Volume 3, 175-9 Publisher:  
Verlag Chemie, Weinheim, Fed. Rep. Ger.  
CODEN: 55BBA6  
DT Conference  
LA English  
CC 3-4 (Biochemical Genetics)  
AB As a 1st step towards the cloning and expression of the xylose isomerase  
[9023-82-9] **gene** of Bacillus subtilis in Saccharomyces  
cerevisiae, a **DNA** fragment for B. subtilis was isolated which  
encodes xylose isomerase and **xylulokinase** [9030-58-4  
]. The **DNA** fragment was cloned on recombinant **plasmids**  
and used to transform an Escherichia coli strain that was isomerase  
deficient. The **plasmids** pMW1 and pMW11 were largely identical

except for a region of .apprx.1 kilobase absent from pMW11. Plasmid pMW11 contained the originally cloned B. subtilis DNA fragment which had been changed in pMW1 by the addition of an insertion element. The presence of pMW1 in E. coli transformants led to wild-type levels of isomerase activity, whereas in pMW11 transformants almost no activity could be detected. Thus, the expression of the B. subtilis gene was observed only after the insertion of an IS element. Furthermore, the expression of the xylose isomerase from pMW1 was not subjected to regulation in the E. coli transformants. The transformants also expressed high levels of **xylulokinase**.

ST xylose isomerase gene Bacillus cloning; yeast xylose  
fermn cloning  
IT Escherichia coli  
(cloning in, of xylose isomerase and **xylulokinase**  
**genes** of Bacillus subtilis)  
IT **Gene** and Genetic element, microbial  
RL: BIOL (Biological study)  
(for xylose isomerase and **xylulokinase**, of Bacillus subtilis,  
cloning and expression in Escherichia coli of)  
IT Molecular cloning  
(of xylose isomerase and **xylulokinase genes**, of  
Bacillus subtilis in Escherichia coli)  
IT Bacillus subtilis  
(xylose isomerase and **xylulokinase genes** of,  
cloning in Escherichia coli of)  
IT **Gene** and Genetic element, microbial  
(insertion sequence, xylose isomerase gene containing, of  
Bacillus subtilis, Escherichia coli expression of)  
IT **Plasmid** and Episome  
(pMW1, xylose isomerase and **xylulokinase genes** of  
Bacillus subtilis cloning on, for expression in Escherichia coli)  
IT 9023-82-9 9030-58-4  
RL: PRP (Properties)  
(gene for, of Bacillus subtilis, cloning and expression in  
Escherichia coli of)

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L66 ANSWER 1 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN 2003-748653 [70] WPIX  
 DNC C2003-205320  
 TI Improvement of ethanol production from xylose employs strain of **Saccharomyces cerevisiae** additionally comprising specific **genes** that are over-expressed.  
 DC D16 E17 H06  
 IN HAHN-HAEGGERDAL, B; JOENSSON, L; WAHLBOM, F  
 PA (FORS-N) FORSKARPATENT I SYD AB  
 CYC 102  
 PI WO 2003078642 A1 20030925 (200370)\* EN 28p C12P007-10  
 RW: AT BE BG CH CY CZ DE DK EA EE ES FI FR GB GH GM GR HU IE IT KE LS  
 LU MC MW MZ NL OA PT RO SD SE SI SK SL SZ TR TZ UG ZM ZW  
 W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK  
 DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR  
 KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT  
 RO RU SC SD SE SG SK SL TJ TM TN TR TT TZ UA UG US UZ VC VN YU ZA  
 ZM ZW  
 ADT WO 2003078642 A1 WO 2003-SE397 20030311  
 PRAI SE 2002-855 20020319  
 IC ICM C12P007-10  
 ICS C12N001-19  
 AB WO2003078642 A UPAB: 20031030  
 NOVELTY - Improving ethanol production from xylose employs strain of **Saccharomyces cerevisiae** additionally comprising over-expressed PET18 (YCR020c), HXT5 (YHR096c), GAL2 (YLR081w), SOL3 (YHR163w), GND1 (YHR183w), TAL1 (YLR354c), TKL1 (YPR074c), PCK1 (YKR097w), ICL1 (YER065c), MLS1 (YNL117w), GAL1 (YBR020c), GAL7 (YBR018c), GAL10 (YBR019c), and/or CAT8 (YMR280c) **genes**. Open reading frames are given in brackets.  
 DETAILED DESCRIPTION - Improving ethanol production from xylose employs strain of **Saccharomyces cerevisiae** comprising **genes** for over-expression of **xylose reductase**, **xylitol dehydrogenase** and **xylulokinase** and additionally over-expressed PET18 (YCR020c), HXT5 (YHR096c), GAL2 (YLR081w), SOL3 (YHR163w), GND1 (YHR183w), TAL1 (YLR354c), TKL1 (YPR074c), PCK1 (YKR097w), ICL1 (YER065c), MLS1 (YNL117w), GAL1 (YBR020c), GAL7 (YBR018c), GAL10 (YBR019c), and/or CAT8 (YMR280c) **genes**. Open reading frames are given in brackets.  
 USE - For improving ethanol production from xylose.  
 ADVANTAGE - The invention improves xylose utilization.  
 Dwg.0/0  
 FS CPI  
 FA AB; DCN  
 MC CPI: D05-B03; E10-E04E2; E11-M; H06-B  
 TECH UPTX: 20031030  
 TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: TEC1 (YBR083w), ARR1 (YPR199c), MIG1 (YGL035c), and/or MIG2 (YGL209w) are deleted. One or more of the **genes** is over expressed and one or more of the **genes** is deleted.

L66 ANSWER 2 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN 2002-097582 [13] WPIX  
 DNC C2002-030382  
 TI Obtaining recombinant **yeast** of **Saccharomyces cerevisiae** for fermenting lignocellulose raw materials to ethanol, comprises introducing **deoxyribonucleic acid** into **yeast**.  
 DC D16 D17 E17  
 IN CORDERO OTERO, R R; HAHN-HAEGGERDAL, B; VAN ZYL, W H; HAHN-HAGERDAL, B; HAHNAEGGERDAL, B

PA (FORS-N) FORSKARPATENT I SYD; (FORS-N) FORSKARPATENT I SYD AB; (OTER-I) CORDERO OTERO R R; (HAHN-I) HAHN-HAGERDAL B; (VZYL-I) VAN ZYL W H

CYC 96

PI WO 2001088094 A1 20011122 (200213)\* EN 18p C12N001-19  
 RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ  
 NL OA PT SD SE SL SZ TR TZ UG ZW  
 W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK  
 DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ  
 LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD  
 SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW  
 AU 2001058985 A 20011126 (200222) C12N001-19  
 EP 1282686 A1 20030212 (200312) EN C12N001-19  
 R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT  
 RO SE SI TR  
 US 2003157675 A1 20030821 (200356) C12P007-06  
 ZA 2002009448 A 20031231 (200408) 29p C12N000-00

ADT WO 2001088094 A1 WO 2001-SE1061 20010515; AU 2001058985 A AU 2001-58985  
 20010515; EP 1282686 A1 EP 2001-932462 20010515, WO 2001-SE1061 20010515;  
 US 2003157675 A1 Cont of WO 2001-SE1061 20010515, US 2002-293255 20021114;  
 ZA 2002009448 A ZA 2002-9448 20021120

FDT AU 2001058985 A Based on WO 2001088094; EP 1282686 A1 Based on WO  
 2001088094

PRAI ZA 2000-2363 20000515

IC ICM C12N000-00; C12N001-19; C12P007-06  
 ICS C12N001-18; C12N015-74; C12P007-10

AB WO 200188094 A UPAB: 20020226  
 NOVELTY - Obtaining recombinant **yeast** of **Saccharomyces cerevisiae**, comprising introducing **DNA** into a **yeast**, where the obtained **yeast** introduces **genes** encoding **xylose reductase**, **xylitol dehydrogenase** and **xylulokinase**, is new.  
 USE - For obtaining recombinant **yeast** of **Saccharomyces cerevisiae** useful for fermenting lignocellulose raw materials to produce ethanol.  
 ADVANTAGE - The obtained recombinant **yeast** is efficiently capable of fermenting lignocellulose raw materials to produce ethanol.  
 Dwg.0/2

FS CPI  
 FA AB; DCN  
 MC CPI: D05-B03; D05-C03B; D05-H05; D05-H08;  
 D05-H12A; D05-H17A3; E10-E04E2

TECH UPTX: 20020226  
 TECHNOLOGY FOCUS - BIOLOGY - Preferred Product: The **yeast** is capable of producing one or more lignocellulose utilizing enzymes of **xylose reductase**, **xylitol dehydrogenase**, or **xylulokinase**. Preferred Enzymes: The enzymes of the **yeast** is of the genus **Saccharomyces cerevisiae** and **Pichia stipitis**. The **xylose reductase** or **xylitol dehydrogenase** lignocellulose utilizing enzyme can be obtained from **Pichia stipitis**. The **xylulokinase** enzyme is obtained from **Saccharomyces cerevisiae**. Preferred Medium: The growth medium by the recombinant **yeast** comprises glucose and xylose. Preferred Method: The method includes isolating mutants by ethyl methanesulfonate treatment. The mutants show a growth rate over basic strain of more than 30%. The recombinant strain is maintained in continuous culture on xylose as carbon source at dilution rate of 0.1/h with growth rate on xylose of 0.14-0.15/h and biomass yield of 0.4 g/g on xylose at aerobic growth. It utilizes 20 g/L and 15-16 g/L of xylose (4-5 g/L residual) in a continuous culture from a 20 g/L xylose and 20 g/L of glucose feed. Preferred Strain: The **Saccharomyces cerevisiae** strain is **Saccharomyces cerevisiae** USM21, which has been deposited under CBS 102678. It is (non-)detoxified lignocellulose hydrolysates, or (soft or hard)wood derived hydrolysate. Preferred Mutants: The mutant is a xylose-fermenting

mutant XYLUSM125, which is deposited under CBS 102679 or XYLUSM145, which is deposited under CBS 102680.

ABEX UPTX: 20020226

EXAMPLE - XYLUSM125 mutant was grown in 20 g/L xylose in minimal medium and established XYLUSM125 in a continuous culture on 20 g/L xylose using dilution rate of 0.1/h (aerobic fermentation condition). The growth rate obtained on xylose as carbon source was 0.14-0.15/h and the biomass yield was 0.4 g/g to have 8 g/L biomass on 20 g/L xylose as carbon source. When the feed was changed to 20 g/L xylose and 20 g/L glucose the biomass had raised to 18 g/L and the result was only 4-5 g/L xylose remained. The XYLUSM125 mutant utilized 20 g/L glucose and 15-16 g/L xylose in continuous fermentation.

L66 ANSWER 3 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN 2002-097498 [13] WPIX

DNC C2002-030322

TI Site-specific insertion in *Zymomonas mobilis*, comprises transforming *Zymomonas* through homologous recombination with **deoxyribonucleic acid** fragment having interrupted sequence.

DC D16 E17

IN CHOU, Y; ZHANG, M

PA (MIDE) MIDWEST RES INST

CYC 95

PI WO 2001083784 A2 20011108 (200213)\* EN 27p C12N015-63

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ  
NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CH CN CO CR CU CZ DE DK DM  
DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC  
LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE  
SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW

CA 2304927 A1 20011102 (200213) EN C12N001-21

AU 2001051397 A 20011112 (200222) C12N015-63

JP 2003531620 W 20031028 (200373) 33p C12N015-09

EP 1366178 A2 20031203 (200380) EN C12N015-90

R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT  
RO SE SI TR

BR 2001010676 A 20031230 (200409) C12N015-63

ADT WO 2001083784 A2 WO 2001-US11239 20010406; CA 2304927 A1 CA 2000-2304927  
20000502; AU 2001051397 A AU 2001-51397 20010406; JP 2003531620 W JP  
2001-580391 20010406; WO 2001-US11239 20010406; EP 1366178 A2 EP  
2001-924773 20010406; WO 2001-US11239 20010406; BR 2001010676 A BR  
2001-10676 20010406; WO 2001-US11239 20010406

FDT AU 2001051397 A Based on WO 2001083784; JP 2003531620 W Based on WO  
2001083784; EP 1366178 A2 Based on WO 2001083784; BR 2001010676 A Based on  
WO 2001083784

PRAI CA 2000-2304927 20000502; US 2000-562613 20000501

IC ICM C12N001-21; C12N015-09; C12N015-63; C12N015-90

ICS C12N015-11

AB WO 200183784 A UPAB: 20020226

NOVELTY - Site-specific insertion in *Zymomonas*, comprising interrupting a sequence in a *Zymomonas* **deoxyribonucleic acid (DNA)** fragment and transforming the *Zymomonas* through homologous recombination with the interrupted fragment, is new.

USE - For insertion inactivation of specific **gene** products in recombinant *Z. mobilis* strains which ferment xylose and/or arabinose into ethanol.

ADVANTAGE - The method eliminates the formation of by-products in a *Z. mobilis* fermentation through the construction of stable recombinant strains to be eliminated.

Dwg.0/10

FS CPI

FA AB; DCN

MC CPI: D05-B03; D05-H05; D05-H09; D05-H12A;

D05-H17A6; E10-E04E2

TECH

UPTX: 20020226

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Method: Interrupting is by inserting a **DNA** sequence inside the **DNA** fragment or by deleting a **DNA** sequence inside the **DNA** fragment. The **DNA** fragment (e.g., **ldh**) is encoding a structural protein in a metabolic pathway of the by-product (e.g., lactic acid) to be eliminated. The interrupted **DNA** fragment is ligated with a **plasmid** vector. Transforming the *Zymomonas mobilis* organism is through homologous recombination with the interrupted fragment of the **plasmid** vector. The *Z. mobilis* of the **plasmid** is cured.

TECHNOLOGY FOCUS - BIOLOGY - Preferred **Plasmid**: The **plasmid** is pZB101, pZB102 or pZB121. It may be pZB1962-ldhL-ara. Preferred Insertion: The insertion is **ldhL**, a selection marker or an operon. The operon encodes structural **gene(s)** including xylose isomerase, **xytulokinase**, L-arabinose isomerase, L-ribulokinase, L-ribulose-5-phosphate-4-epimerase, transaldolase or transketolase, and a promoter for expression of the structural **gene** in *Z. mobilis*.

ABEX

UPTX: 20020226

EXAMPLE - **Plasmids** containing **ldh gene** of *Zymomonas* having a tetracycline (Tc) resistant **gene** insert (**ldh::Tc**) cassette were used to transform *Z. mobilis*. The resultant Tc resistance transformants were analyzed by Southern hybridization. Results showed that the **ldh::Tc** cassette had been inserted into the **ldh** region of the *Zymomonas* genome. The **gene** integration based on homologous recombination in *Zymomonas*, together with the targeted integration resulting in an inactivated **ldh gene**, eliminated lactic acid by-product formation in ethanol fermentation.

L66 ANSWER 4 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN 2002-089743 [12] WPIX

CR 2003-731102 [69]

DNC C2002-027635

TI Transposon for **plasmid** vector for constructing strains of *Zymomonas mobilis* for conversion of pentose sugars into ethanol, comprises operon(s) having structural **genes** encoding enzymes and promoter(s).

DC D16 E17 H06

IN CHOU, Y; ZHANG, M

PA (MIDE) MIDWEST RES INST; (CHOU-I) CHOU Y; (ZHAN-I) ZHANG M

CYC 96

PI WO 2001083786 A2 20011108 (200212)\* EN 49p C12N015-74

RW: AT BE CH CY DE DK EA ES FI FR GB GH GM GR IE IT KE LS LU MC MW MZ  
NL OA PT SD SE SL SZ TR TZ UG ZW

W: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CH CN CO CR CU CZ DE DK DM  
DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC  
LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE  
SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW

CA 2304929 A1 20011102 (200212) EN C12N001-21

AU 2001049926 A 20011112 (200222) C12N015-74

US 2002151034 A1 20021017 (200270) C12N001-20

EP 1278876 A2 20030129 (200310) EN C12N015-74

R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT  
RO SE SI TR

ADT WO 2001083786 A2 WO 2001-US11334 20010406; CA 2304929 A1 CA 2000-2304929  
20000502; AU 2001049926 A AU 2001-49926 20010406; US 2002151034 A1 US  
2000-565233 20000501; EP 1278876 A2 EP 2001-923213 20010406, WO  
2001-US11334 20010406

FDT AU 2001049926 A Based on WO 2001083786; EP 1278876 A2 Based on WO  
2001083786

PRAI CA 2000-2304929 20000502; US 2000-565233 20000501

IC ICM C12N001-20; C12N001-21; C12N015-74



ICS C12N015-09; C12N015-11; C12N015-52; C12N015-63; C12N015-90;  
C12P007-04; C12P007-06

AB WO 200183786 A UPAB: 20031027

NOVELTY - A transposon for stable insertion of foreign **genes** into a bacterial genome, comprising operon(s) having xylA/xylB, araBAD or tal/tkt as structural **genes** encoding enzymes, and promoter(s) for expression of the structural **genes** in the bacterium, where the operons are contained inside a pair of inverted insertion sequences, and a transposase **gene** is located outside of the insertion sequences, is new.

USE - The transposon, e.g., Tn5 or Tn10 derivative, is for a **plasmid** vector (e.g., pZB1862-ldhL-ara ATCC Accession Number PTA-1798) which transforms a bacterium, i.e. Zymomonas mobilis (claimed). The strains of Z. mobilis (e.g., G8 ATCC Accession Number PTA-1796, C25 ATCC Accession Number PTA-1799, and AX ATCC Accession Number PTA-1797) are useful in the conversion of the cellulose derived pentose sugars, e.g., xylose and arabinose, into fuels and chemicals, e.g. ethanol.

ADVANTAGE - The invention provides for the construction of Z. mobilis strains which are capable of fermenting xylose and/or arabinose to ethanol through the generation of stable genomic inserts which encode the enzymes necessary for xylose and arabinose catabolism. The strains are free of antibiotic resistance and stable for more than 40 (at least 45) generations in a non-selection media. The strains also demonstrate a high specific rate of product formation at close to maximum theoretical product yield.

Dwg.0/18

FS CPI

FA AB; DCN

MC CPI: D05-B03; D05-C07; **D05-H12D5**; **D05-H12E**; E10-E04L2;  
H06-B

TECH UPTX: 20020221

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Component: The promoter is Peno or Pgap.

ABEX UPTX: 20020221

EXAMPLE - Two operons containing Pgap-xylA/xylB and Peno-talB/tktA were assembled in mini-Tn5 and the resulting **plasmid** was conjugated into Z. mobilis. With the help of the transposase located outside of the mini-Tn5 cassette, single copies of the two operons were inserted into the Z. mobilis genome. Enzymatic analysis of xylose isomerase, **xylulokinase**, transaldolase, and transketolase indicated that all the **genes** coordinately expressed and that the integrated strains produced 30-70% of the enzymatic activities of the **plasmid**-bearing strains. These enzymatic levels were enough for the organism to grow and ferment xylose to ethanol.

L66 ANSWER 5 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN 2000-526176 [48] WPIX

DNC C2000-156444

TI **Genetically** modified microorganism useful for producing xylitol from D-xylulose comprises an exogenous **xylitol dehydrogenase gene**.

DC B05 D13 D16 D17 E17

IN TAKENAKA, Y; TONOUCHI, N; YOKOZEKI, K

PA (AJIN) AJINOMOTO KK; (AJIN) AJINOMOTO CO INC

CYC 30

PI EP 1029925 A1 20000823 (200048)\* EN 21p C12P007-18

R: AL AT BE CH CY DE DK ES FI FR GB GR IE IT LI LT LU LV MC MK NL PT  
RO SE SI

|                  |                   |     |            |
|------------------|-------------------|-----|------------|
| JP 2000295994 A  | 20001024 (200059) | 16p | C12N015-09 |
| CN 1271017 A     | 20001025 (200104) |     | C12P007-18 |
| KR 2000076625 A  | 20001226 (200134) |     | C12N001-00 |
| BR 2000000338 A  | 20010821 (200155) |     | C12P007-18 |
| US 2003148482 A1 | 20030807 (200358) |     | C12P007-18 |

ADT EP 1029925 A1 EP 2000-102566 20000207; JP 2000295994 A JP 1999-197621  
19990712; CN 1271017 A CN 2000-105396 20000209; KR 2000076625 A KR  
2000-5838 20000208; BR 2000000338 A BR 2000-338 20000208; US 2003148482 A1  
Cont of US 2000-500908 20000209, US 2002-277706 20021023

PRAI JP 1999-197621 19990712; JP 1999-31464 19990209

IC ICM C12N001-00; C12N015-09; C12P007-18

ICS C12N001-20; C12N009-04; C12N015-00; C12N015-74

ICA C12N001-21

AB EP 1029925 A UPAB: 20001001

NOVELTY - Microorganism (I) that has been transformed with a **gene** encoding **xylitol dehydrogenase** (XDH) and is capable of supplying reducing power to its culture medium (i.e. of producing sufficient reduced nicotinamide adenine **dinucleotide** (NADH) for XDH-catalyzed conversion of D-xylulose to xylitol) is new.

DETAILED DESCRIPTION - An INDEPENDENT CLAIM is also included for a process for producing xylitol by reacting a microorganism of type (I) with D-xylulose and collecting the resulting xylitol.

USE - The xylitol is useful as a low-calorie, non-carcinogenic sweetener and for fluid therapy in the treatment of diabetes.

ADVANTAGE - (I) is capable of converting D-xylulose to xylitol in the absence of added carbon sources or NADH.

Dwg.0/0

FS CPI

FA AB; DCN

MC CPI: B04-F10A3E; B10-A07; B14-S04; D03-H01A; D05-C03B; D05-C08;  
**D05-H12A; D05-H14A1; D05-H17A3; D06-G;**  
E10-A07

TECH UPTX: 20001001

TECHNOLOGY FOCUS - BIOTECHNOLOGY - Preferred Process: The D-xylulose is produced by means of a microorganism (II) capable of converting D-arabitol to D-xylulose or a microorganism (III) capable of producing D-xylulose from glucose. Preferred Microorganisms: (I) is an *Escherichia coli* transformant. (II) is a microorganism of the genus *Gluconobacter*, *Achromobacter*, *Agrobacterium*, *Alcaligenes*, *Arthrobacter*, *Azotobacter*, *Brevibacterium*, *Corynebacterium*, *Enterobacter*, *Erwinia*, *Flavobacterium*, *Micrococcus*, *Morganella*, *Nocardia*, *Planococcus*, *Proteus*, *Propionibacterium*, *Pseudomonas*, *Rhodococcus*, *Sporosarcina*, *Staphylococcus*, *Vibrio*, *Actinomadura*, *Actinomyces*, *Kitasatosporia*, *Streptomyces*, *Aeromonas*, *Aureobacterium*, *Bacillus*, *Escherichia*, *Microbacterium*, *Serratia*, *Salmonella* or *Xanthomonas*. (III) is a microorganism of the genus *Gluconobacter*, *Acetobacter* or *Frateuria*.

ABEX UPTX: 20001001

EXAMPLE - A 1.2 kilobase XDH **DNA** fragment was amplified from *Morganella morganii* genomic **DNA**, digested with *EcoRI* and *BamHI*, and ligated into *EcoRI*/*BamHI*-digested pUC18. The product was used to transform *Escherichia coli* JM109. The transformants were cultured overnight in L medium (1 percent tryptone, 0.5 percent **yeast** extract, 0.5 percent sodium chloride). The cultures were sonicated and the supernatants (100 microliters) were incubated at 30 degrees Centigrade for 1 minute in a reaction mixture (1 milliliter) containing 100 milliMolar glycine buffer (pH 9.5), 100 milliMolar xylitol and 2 milliMolar nicotinamide adenine **dinucleotide**. One transformant had an **xylitol dehydrogenase** activity of 3.9 Units/milligram (1 unit being the activity required for oxidizing 1 micromole of xylitol to generate 1 micromole of NADH per minute).

L66 ANSWER 6 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN 1997-558974 [51] WPIX

DNC C1997-178545

TI **Yeast** which ferments xylose to ethanol - comprising xylitol reductase, **xylitol dehydrogenase** and **xylulokinase genes** integrated at each of its multiple reiterated ribosomal **DNA** sites.

DC D16 D17 E17 H06  
 IN CHEN, Z; HO, N W Y  
 PA (PURD) PURDUE RES FOUND  
 CYC 76  
 PI WO 9742307 A1 19971113 (199751)\* EN 66p C12N001-16  
 RW: AT BE CH DE DK EA ES FI FR GB GH GR IE IT KE LS LU MC MW NL OA PT  
 SD SE SZ UG  
 W: AL AM AT AU AZ BA BB BG BR BY CA CH CN CU CZ DE DK EE ES FI GB GE  
 HU IL IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MD MG MK MN MW MX  
 NO NZ PL PT RO RU SD SE SG SI SK TJ TM TR TT UA UG US UZ VN YU  
 AU 9728301 A 19971126 (199813) C12N001-16  
 EP 898616 A1 19990303 (199913) EN C12N001-16  
 R: AT BE DE DK ES FI FR GB GR IE IT NL PT SE  
 CN 1225125 A 19990804 (199949) C12N001-16  
 JP 2000509988 W 20000808 (200043) 50p C12N015-09  
 MX 9809223 A1 19990701 (200061) C12N001-16  
 AU 731102 B 20010322 (200122) C12N001-16  
 BR 9710963 A 20010731 (200146) C12N001-16  
 ADT WO 9742307 A1 WO 1997-US7663 19970506; AU 9728301 A AU 1997-28301  
 19970506; EP 898616 A1 EP 1997-922698 19970506; WO 1997-US7663 19970506;  
 CN 1225125 A CN 1997-196195 19970506; JP 2000509988 W JP 1997-540153  
 19970506; WO 1997-US7663 19970506; MX 9809223 A1 MX 1998-9223 19981105; AU  
 731102 B AU 1997-28301 19970506; BR 9710963 A BR 1997-10963 19970506; WO  
 1997-US7663 19970506  
 FDT AU 9728301 A Based on WO 9742307; EP 898616 A1 Based on WO 9742307; JP  
 2000509988 W Based on WO 9742307; AU 731102 B Previous Publ. AU 9728301,  
 Based on WO 9742307; BR 9710963 A Based on WO 9742307  
 PRAI US 1996-16865P 19960506  
 REP 6.Jnl.Ref; WO 9513362  
 IC ICM C12N001-16; C12N015-09  
 ICS C12N001-18; C12N001-19; C12N015-68; C12N015-69; C12N015-81;  
 C12P007-06  
 ICI C12N001-19; C12N001-19; C12N001-19; C12R001:72; C12R001:84; C12R001:85  
 AB WO 9742307 A UPAB: 19991020  
 Novel **yeast** which ferments xylose to ethanol, comprises: (a)  
**xylose reductase** (XR), **xylitol**  
**dehydrogenase** (XD) and **xylulokinase** (XK) **genes**  
 integrated at each of its multiple reiterated ribosomal **DNA**  
 sites; (b) multiple copies of exogenous **DNA**, including XR, XD,  
 and XK **genes**, fused to non-glucose inhibited promoters  
 integrated into its **chromosomal DNA**, where the  
**yeast** simultaneously ferments glucose and xylose to ethanol; or  
 (c) multiple copies of an introduced **DNA** containing XR, XD and  
 XK **genes**, where the **yeast** ferments xylose to ethanol,  
 where the **yeasts** of (b) and (c) retain their capacity for  
 fermenting xylose to ethanol when cultured under non-selective conditions  
 for at least 20 generations.  
 USE - The methods can produce **yeast**, which even upon  
 culture in non-selective medium for multiple generations, e.g. up to 20,  
 retain their full capability to ferment xylose to ethanol.  
 Dwg.0/12  
 FS CPI  
 FA AB; DCN  
 MC CPI: D05-B03; D05-H12E; D05-H14A2; D06-G; E10-E04E2;  
 H06-B  
 L66 ANSWER 7 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN  
 AN 1995-194082 [25] WPIX  
 DNC C1995-089834  
 TI Recombinant **yeast** encoding **xylose reductase**,  
**xylitol dehydrogenase** and **xylulokinase** - can  
 effectively ferment xylose alone, or simultaneously with glucose, to  
 produce ethanol e.g. for use as a fuel.

DC D16 E17 H06  
 IN HO, N W Y; TSAO, G T  
 PA (PURD) PURDUE RES FOUND  
 CYC 59

PI WO 9513362 A1 19950518 (199525)\* EN 63p C12N001-14  
 RW: AT BE CH DE DK ES FR GB GR IE IT KE LU MC MW NL OA PT SD SE SZ  
 W: AM AU BB BG BR BY CA CN CZ EE FI GE HU JP KG KP KR KZ LK LR LT LV  
 MD MG MN NO NZ PL RO RU SI SK TJ TT UA UZ VN

AU 9510517 A 19950529 (199537) C12N001-14

EP 728192 A1 19960828 (199639) EN C12N001-14

R: AT BE DE DK ES FR GB GR IE IT NL SE

FI 9601926 A 19960704 (199641) C12N000-00

BR 9408010 A 19961217 (199705) C12N001-14

JP 09505469 W 19970603 (199732) 56p C12N015-09

US 5789210 A 19980804 (199838) C12P007-08

AU 695930 B 19980827 (199846) C12N001-14

CN 1141057 A 19970122 (200047) C12N001-14

ADT WO 9513362 A1 WO 1994-US12861 19941108; AU 9510517 A AU 1995-10517  
 19941108; EP 728192 A1 WO 1994-US12861 19941108, EP 1995-901176 19941108;  
 FI 9601926 A WO 1994-US12861 19941108, FI 1996-1926 19960507; BR 9408010 A  
 BR 1994-8010 19941108, WO 1994-US12861 19941108; JP 09505469 W WO  
 1994-US12861 19941108, JP 1995-513948 19941108; US 5789210 A US  
 1993-148581 19931108; AU 695930 B AU 1995-10517 19941108; CN 1141057 A CN  
 1994-194767 19941108

FDT AU 9510517 A Based on WO 9513362; EP 728192 A1 Based on WO 9513362; BR  
 9408010 A Based on WO 9513362; JP 09505469 W Based on WO 9513362; AU  
 695930 B Previous Publ. AU 9510517, Based on WO 9513362

PRAI US 1993-148581 19931108

REP 4.Jnl.Ref

IC ICM C12N000-00; C12N001-14; C12N015-09; C12P007-08

ICS C07H021-04; C12N001-19; C12N009-00; C12N009-02; C12N009-12;  
 C12N015-00; C12N015-81; C12P007-06

ICI C12N015-09, C12R001:865; C12N001-19, C12R001:865; C12P007-06, C12R001:865

AB WO 9513362 A UPAB: 19951128

Recombinant **yeast** (pref. of the genus **Saccharomyces**)  
 contains introduced **genes** (pref. fused to non-glucose-inhibited  
 promoters) encoding **xylose reductase**, **xylitol**  
**dehydrogenase** (XD) and **xylulokinase** effective for  
 fermenting xylose to ethanol. Also claimed are: (1) a recombinant  
**DNA** molecule comprising **genes** encoding **xylose**  
**reductase**, XD and **xylulokinase**; and (2) a vector for  
 transforming **yeast** comprising these **genes**.

USE - The **yeast** can effectively ferment xylose, alone or  
 simultaneously with glucose, to produce ethanol; the ethanol can be used  
 as liquid fuel for cars either as a neat fuel (100% ethanol) or as a blend  
 with petroleum.

ADVANTAGE - The recombinant **yeast** are suitable for ethanol  
 fuel production by fermentation using plant biomass as feedstock.

Dwg.0/14

FS CPI

FA AB; GI; DCN

MC CPI: D05-B03; D05-H12C; D05-H12E; D05-H14A2;  
 D06-B; E10-E04E2; E11-N; H06-B

L66 ANSWER 8 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN 1994-167479 [20] WPIX

CR 2001-465360 [50]; 2003-777185 [73]

DNC C1994-076813

TI Production of xylitol from recombinant hosts - using a metabolic pathway which  
 uses a carbon source other than D-xylose, D-xylulose or their oligomers.

DC B05 D13 D16 E17

IN APAJALAHTI, J H A; HARKKI, A M; MYASNIKOV, A N; PASTINEN, O A; APAJALAHTI,  
 J; HARKKI, A; MYASNIKOV, A; PASTINEN, O; APAJALAHTI, J H; MJASNIKOV, A N;

NOVOMIROVICH, A; ANDREI, N M  
 PA (XYRO-N) XYROFIN OY  
 CYC 47  
 PI WO 9410325 A1 19940511 (199420)\* EN 90p C12P007-18  
 RW: AT BE CH DE DK ES FR GB GR IE IT LU MC NL OA PT SE  
 W: AT AU BB BG BR BY CA CH CZ DE DK ES FI GB HU JP KP KR KZ LK LU LV  
 MG MN MW NL NO NZ PL PT RO RU SD SE SK UA US UZ VN  
 AU 9454215 A 19940524 (199434) C12P007-18  
 NO 9501747 A 19950705 (199538) C12P007-18  
 FI 9502148 A 19950704 (199540) C12N000-00  
 EP 672161 A1 19950920 (199542) EN C12P007-18  
 R: AT BE CH DE DK ES FR GB GR IE IT LI LU NL PT SE  
 NZ 257561 A 19960925 (199644) C12P007-18  
 JP 08505522 W 19960618 (199648) 88p C12N015-09  
 US 5631150 A 19970520 (199726) 34p C12P019-02  
 HU 72187 T 19960328 (199741) C12P007-18  
 EP 672161 B1 19990922 (199943) EN C12P007-18  
 R: AT BE CH DE DK ES FR GB GR IE IT LI LU NL PT SE  
 DE 69326559 E 19991028 (199951) C12P007-18  
 BR 9307391 A 19990831 (200002) C12P007-18  
 ES 2139024 T3 20000201 (200013) C12P007-18  
 RU 2142999 C1 19991220 (200043) C12N015-52  
 HU 219016 B 20010131 (200112) C12P007-18  
 FI 108300 B1 20011231 (200214) C12P007-18  
 JP 3433295 B2 20030804 (200354) 39p C12N015-09  
 ADT WO 9410325 A1 WO 1993-FI450 19931105; AU 9454215 A WO 1993-FI450 19931105,  
 AU 1994-54215 19931105; NO 9501747 A WO 1993-FI450 19931105, NO 1995-1747  
 19950504; FI 9502148 A WO 1993-FI450 19931105, FI 1995-2148 19950504; EP  
 672161 A1 EP 1993-924615 19931105, WO 1993-FI450 19931105; NZ 257561 A NZ  
 1993-257561 19931105, WO 1993-FI450 19931105; JP 08505522 W WO 1993-FI450  
 19931105, JP 1994-510748 19931105; US 5631150 A CIP of US 1992-973325  
 19921105, Cont of US 1993-110672 19930824, US 1995-368395 19950103; HU  
 72187 T WO 1993-FI450 19931105, HU 1995-1288 19931105; EP 672161 B1 EP  
 1993-924615 19931105, WO 1993-FI450 19931105; DE 69326559 E DE 1993-626559  
 19931105, EP 1993-924615 19931105, WO 1993-FI450 19931105; BR 9307391 A BR  
 1993-7391 19931105, WO 1993-FI450 19931105; ES 2139024 T3 EP 1993-924615  
 19931105; RU 2142999 C1 WO 1993-FI450 19931105, RU 1995-113172 19931105;  
 HU 219016 B WO 1993-FI450 19931105, HU 1995-1288 19931105; FI 108300 B1 WO  
 1993-FI450 19931105, FI 1995-2148 19950504; JP 3433295 B2 WO 1993-FI450  
 19931105, JP 1994-510748 19931105  
 FDT AU 9454215 A Based on WO 9410325; EP 672161 A1 Based on WO 9410325; NZ  
 257561 A Based on WO 9410325; JP 08505522 W Based on WO 9410325; HU 72187  
 T Based on WO 9410325; EP 672161 B1 Based on WO 9410325; DE 69326559 E  
 Based on EP 672161, Based on WO 9410325; BR 9307391 A Based on WO 9410325;  
 ES 2139024 T3 Based on EP 672161; RU 2142999 C1 Based on WO 9410325; HU  
 219016 B Previous Publ. HU 72187, Based on WO 9410325; FI 108300 B1  
 Previous Publ. FI 9502148; JP 3433295 B2 Previous Publ. JP 08505522, Based  
 on WO 9410325  
 PRAI US 1992-973325 19921105; US 1993-110672 19930824; US 1995-368395  
 19950103  
 REP 01Jnl.Ref; EP 450430; WO 9115588  
 IC ICM C12N000-00; C12N015-09; C12N015-52; C12P007-18; C12P019-02  
 ICS C12N001-15; C12N001-19; C12N005-10; C12P019-00  
 AB WO 9410325 A UPAB: 20031112  
 Production of xylitol from a recombinant host comprises (a) constructing  
 within a microbial host, a novel metabolic pathway leading to the  
 synthesis of xylitol as an end prod. from a carbon source other than  
 D-xylose, D-xylulose or polymers or oligomers containing D-xylose or  
 D-xylulose as major components, (b) growing the recombinant host under  
 conditions that provide for the synthesis of the xylitol using the pathway  
 and on a carbon source other than those in (a), and (c) recovering the  
 xylitol. Pref. the recombinant host may be transformed with a  
 construct-encoding enzymes such as D-glucose-6-phosphate dehydrogenase

(GPD), 6-phospho-D-gluconate dehydrogenase (PGD), D-ribulose-5-phosphate-3-epimerase (RPE), D-ribulokinase (RK), **xylitol dehydrogenase** (XD) and D-arabitol dehydrogenase (AD).

USE/ADVANTAGE - The xylitol produced is used as a sweetener. The method can be used to produce xylitol using readily available sources such as D-glucose.

Dwg.0/0

FS

CPI

FA

AB; DCN

MC

CPI: B04-F09; B10-E04C; B11-A01; B14-E11; D03-H01A; D05-C08;  
D05-H14A; D05-H17A3; E10-A07

ABEQ

US 5631150 A UPAB: 19970626

A method for production of xylitol from a recombinant microbial host, comprises:

a) growing an arabitol-producing **yeast** or an arabitol-producing fungus under conditions that provide for the synthesis of xylitol, where the arabitol-producing **yeast** or arabitol-producing fungus has been modified to synthesize xylitol as an end product in a fermentation when grown on D-arabitol or a carbon source that the unmodified arabitol-producing **yeast** or unmodified arabitol-producing fungus utilized for D-arabitol biosynthesis, the carbon source being other than D-xylose, D-xylulose, mixtures of D-xylose and D-xylulose, and polymers and oligomers containing D-xylose or D-xylulose as major components under conditions that provide for synthesis of xylitol where before the modification the host produced D-arabitol but did not utilize D-arabitol for the synthesis of xylitol, and the host has been transformed with a **DNA** encoding a D-xylulose forming D-arabitol dehydrogenase (E.C. 1.1.1.11) and with a **DNA** encoding **xylitol dehydrogenase** (E.C. 1.1.1.9); and

b) recovering the xylitol produced in step a.

Dwg.0/11

L66 ANSWER 9 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN 1991-325230 [44] WPIX

DNC C1991-140554

TI **DNA** encoding **xylose reductase** and/or **xylitol dehydrogenase** - useful for transforming **yeast** strains for expression of one enzyme or co-expression of both.

DC B05 D13 D16 E17 F09

IN AIRAKSINEN, U; HAHN-HAGERDAL, B; HALLBORN, J; KERANEN, S; OJAMO, H; PENTTILA, M; WALFRIDSSON, M; HAHN-HAEGERDAL, B; KERAENEN, S; PENTTILAE, M; HAHNHAGERD, B; WALFRIDSSO, M

PA (VALW) VALTION TEKNILLINEN TUTKIMUSKESKUS; (XYRO-N) XYROFIN OY; (VALW) VALTION TEKNILLINEN; (HALL-I) HALLBORN J

CYC 20

PI WO 9115588 A 19911017 (199144)\* 47p  
RW: AT BE CH DE DK ES FR GB GR IT LU NL SE  
W: AU CA FI JP NO US

|  |    |          |          |                   |
|--|----|----------|----------|-------------------|
| AU 9175657                                   | A  | 19911030 | (199205) |                   |
| FI 9204461                                   | A  | 19921002 | (199302) | C12N000-00        |
| NO 9203880                                   | A  | 19921006 | (199306) | C12N015-53        |
| EP 527758                                    | A1 | 19930224 | (199308) | EN C12N015-53     |
| R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE |    |          |          |                   |
| JP 05507843                                  | W  | 19931111 | (199350) | 17p C12N015-53    |
| AU 647104                                    | B  | 19940317 | (199416) | C12N015-53        |
| EP 527758                                    | B1 | 19980107 | (199806) | EN 24p C12N015-53 |
| R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE |    |          |          |                   |
| DE 69128619                                  | E  | 19980212 | (199812) | C12N015-53        |
| ES 2113373                                   | T3 | 19980501 | (199824) | C12N015-53        |
| US 5866382                                   | A  | 19990202 | (199912) | C12P007-02        |
| FI 9902153                                   | A  | 19991006 | (200003) | C12N000-00        |
| FI 104636                                    | B1 | 20000315 | (200020) | C12N015-53        |

NO 308544 B1 20000925 (200056) C12N015-53  
 CA 2090122 C 20020618 (200250) EN C12N015-53  
 JP 3348215 B2 20021120 (200282) 21p C12P007-18  
 US 6582944 B1 20030624 (200343) C12P007-06  
 FI 112250 B1 20031114 (200377) C12P007-06

ADT FI 9204461 A WO 1991-FI103 19910408, FI 1992-4461 19921002; NO 9203880 A  
 WO 1991-FI103 19910408, NO 1992-3880 19921006; EP 527758 A1 EP 1991-906996  
 19910408, WO 1991-FI103 19910408; JP 05507843 W JP 1991-506907 19910408,  
 WO 1991-FI103 19910408; AU 647104 B AU 1991-75657 19910408; EP 527758 B1  
 EP 1991-906996 19910408, WO 1991-FI103 19910408; DE 69128619 E DE  
 1991-628619 19910408, EP 1991-906996 19910408, WO 1991-FI103 19910408; ES  
 2113373 T3 EP 1991-906996 19910408; US 5866382 A CIP of US 1990-527775  
 19900524, Cont of US 1992-848694 19920309, US 1994-336198 19941103; FI  
 9902153 A WO 1991-FI103 19910408, Div ex FI 1992-4461 19921002, FI  
 1999-2153 19991006; FI 104636 B1 WO 1991-FI103 19910408, FI 1992-4461  
 19921002; NO 308544 B1 WO 1991-FI103 19910408, NO 1992-3880 19921006; CA  
 2090122 C CA 1991-2090122 19910408, WO 1991-FI103 19910408; JP 3348215 B2  
 JP 1991-506907 19910408, WO 1991-FI103 19910408; US 6582944 B1 CIP of US  
 1990-527775 19900524, CIP of WO 1991-FI103 19910408, Cont of US  
 1992-848694 19920309, Div ex US 1994-336198 19941103, US 1999-184965  
 19990108; FI 112250 B1 WO 1991-FI103 19910408, Div ex FI 1992-4461  
 19921002, FI 1999-2153 19991006

FDT EP 527758 A1 Based on WO 9115588; JP 05507843 W Based on WO 9115588; AU  
 647104 B Previous Publ. AU 9175657, Based on WO 9115588; EP 527758 B1  
 Based on WO 9115588; DE 69128619 E Based on EP 527758, Based on WO  
 9115588; ES 2113373 T3 Based on EP 527758; FI 104636 B1 Previous Publ. FI  
 9204461; NO 308544 B1 Previous Publ. NO 9203880; CA 2090122 C Based on WO  
 9115588; JP 3348215 B2 Previous Publ. JP 05507843, Based on WO 9115588; US  
 6582944 B1 Div ex US 5866382; FI 112250 B1 Previous Publ. FI 9902153

PRAI FI 1990-1771 19900406

REP 7.Jnl.Ref

IC ICM C12N000-00; C12N015-53; C12P007-02; C12P007-06; C12P007-18  
 ICS C07H021-04; C12N001-15; C12N001-19; C12N009-02; C12N015-52;  
 C12N015-81; C12P019-02

ICA C12N009-04; C12N015-09

ICI C12P007-18, C12R001:865

AB WO 9115588 A UPAB: 20040123

**DNA (I) encoding xylose reductase enzyme (A)**  
 is new. When (I) is transferred into a **yeast** strain it renders  
 the strain capable of reducing xylose to xylitol.  
 Pref. the **yeast** of (I) is capable of integrating to the  
**yeast chromosome** when transformed into a **yeast**  
 strain. (I) and/or (II) is expressed under **yeast gene**  
 regulatory regions, e.g. promoters of (A), (B), **yeast alcohol**  
**dehydrogenase gene ADH1** or **yeast phosphoglycerate**  
**kinase gene PGK1**, and functional fragments. The **yeast**  
 strain is a **Saccharomyces cerevisiae** strain (pref.),  
**kluveromyces** strain, **Schizosaccharomyces pombe** strain or **Pichia** strain.  
 The **yeast** vectors pUA103, pUA107, pJHXR22, pMW22, pJHDXDH60  
 and pJHDXDH70, and the **yeast** strains. *S. cerevisiae* H475, H477,  
 H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are  
 specifically claimed.

USE - The **yeast** transformants can reduce xylase to xylitol  
 for use by diabetics or as a natural sweetener. The co-expression of the  
 two enzymes in a **yeast** strain results in the production of ethanol.  
 Dwg. 0/8

FS CPI  
 FA AB; DCN

MC CPI: B04-B02B2; B04-B02C2; B04-B04A1; B10-A07; B10-E04D; B11-A; B12-J01;  
 B12-L03; D05-B03; D05-C03B; D05-C03D; **D05-H03B**;  
**D05-H12**; E10-A07; F05-A02C; F05-B

ABEQ EP 527758 A UPAB: 19930928

**DNA (I) encoding xylose reductase enzyme (A)**

is new. When (I) is transferred into a **yeast** strain it renders the strain capable of reducing xylose to xylitol.

Pref. the **yeast** of (I) is capable of integrating to the **yeast chromosome** when transformed into a **yeast** strain. (I) and/or (II) is expressed under **yeast gene** regulatory regions, e.g. promoters of (A), (B), **yeast** alcohol dehydrogenase **gene** ADH1 or **yeast** phosphoglycerate kinase **gene** PGK1, and functional fragments. The **yeast** strain is a **Saccharomyces cerevisiae** strain (pref.), **kluveromyces** strain, **Schizosaccharomyces pombe** strain or **Pichia** strain.

The **yeast** vectors pUA103, pUA107, pJHXR22, pMW22, pJHDXH60, and pJHDXH70, and the **yeast** strains *S. cerevisiae* H475, H477, H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are specifically claimed.

USE - The **yeast** transformants can reduce xylase to xylitol for use by diabetics or as a natural sweetener. The co-expression of the two enzymes in a **yeast** strain results in the prodn. of ethanol

ABEQ EP 527758 B UPAB: 19980209

**DNA** (I) encoding **xylose reductase** enzyme (A) is new. When (I) is transferred into a **yeast** strain it renders the strain capable of reducing xylose to xylitol.

Pref. the **yeast** of (I) is capable of integrating to the **yeast chromosome** when transformed into a **yeast** strain. (I) and/or (II) is expressed under **yeast gene** regulatory regions, e.g. promoters of (A), (B), **yeast** alcohol dehydrogenase **gene** ADH1 or **yeast** phosphoglycerate kinase **gene** PGK1, and functional fragments. The **yeast** strain is a **Saccharomyces cerevisiae** strain (pref.), **kluveromyces** strain, **Schizosaccharomyces pombe** strain or **Pichia** strain.

The **yeast** vectors pUA103, pUA107, pJHXR22, pMW22, pJHDXH60 and pJHDXH70, and the **yeast** strains *S. cerevisiae* H475, H477, H479, H481, VTT-C-91181, H949, H495, H496, H497, H492 and H493 are specifically claimed.

USE - The **yeast** transformants can reduce xylase to xylitol for use by diabetics or as a natural sweetener. The co-expression of the two enzymes in a **yeast** strain results in the prodn. of ethanol.  
Dwg.0/8

L66 ANSWER 10 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN 1991-296506 [41] WPIX

DNC C1991-128227

TI New **DNA** encoding **xylose reductase** and **xylitol dehydrogenase** - and transformed **yeast** for production of ethanol and biomass from xylose or recovery of oxidised NADP.

DC B02 B04 D16 E17

IN AMORE, R; HAGEDORN, J; HOLLENBERG, C P; KOTTER, P; PIONTEK, M; STRASSER, A W M; VONCIRIACY, M; KOETTER, P; VON, CIRIACY-WANTRUP M; HAGENDORN, J

PA (RHEI-N) RHEIN BIOTECH NEUE BIOTECHNOLOGISCHE PROZESSE & PROD GMBH; (RHEI-N) RHEIN BIOTECH GES NEUE BIOTECHNOLOGISCHE; (RHEI-N) RHEIN BIOTECH GES B; (RHEI-N) RHEIN BIOTECH GMBH

CYC 16

|    |             |    |  |     |            |
|----|-------------|----|--|-----|------------|
| PI | DE 4009676  | A  | 19911002 (199141)*                           | 50p |            |
|    | EP 450430   | A  | 19911009 (199141)                            | 50p |            |
|    |             |    | R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE |     |            |
|    | CA 2039021  | A  | 19910927 (199150)                            |     |            |
|    | EP 450430   | A3 | 19920102 (199320)                            | 50p |            |
|    | DE 4009676  | C2 | 19930909 (199336)                            | 51p | C12N001-19 |
|    | JP 06339383 | A  | 19941213 (199509)                            | 32p | C12N015-53 |
|    | EP 450430   | B1 | 19970625 (199730)                            | EN  | C12N015-53 |
|    |             |    | R: AT BE CH DE DK ES FR GB GR IT LI LU NL SE |     |            |
|    | DE 69126632 | E  | 19970731 (199736)                            |     | C12N015-53 |
|    | ES 2104626  | T3 | 19971016 (199748)                            |     | C12N015-53 |



JP 2000139486 A 20000523 (200033) 21p C12N015-09  
 JP 3122153 B2 20010109 (200104) 32p C12N015-09  
 JP 2001103988 A 20010417 (200128) 27p C12N015-09  
 JP 3193917 B2 20010730 (200146) 27p C12N015-09  
 ADT DE 4009676 A DE 1990-4009676 19900326; EP 450430 A EP 1991-104558  
 19910322; EP 450430 A3 EP 1991-104558 19910322; DE 4009676 C2 DE  
 1990-4009676 19900326; JP 06339383 A JP 1991-62160 19910326; EP 450430 B1  
 EP 1991-104558 19910322; DE 69126632 E DE 1991-626632 19910322, EP  
 1991-104558 19910322; ES 2104626 T3 EP 1991-104558 19910322; JP 2000139486  
 A Div ex JP 1991-62160 19910326, JP 2000-589 19910326; JP 3122153 B2 JP  
 1991-62160 19910326; JP 2001103988 A Div ex JP 1991-62160 19910326, JP  
 2000-276227 19910326; JP 3193917 B2 Div ex JP 1991-62160 19910326, JP  
 2000-276227 19910326  
 FDT DE 69126632 E Based on EP 450430; ES 2104626 T3 Based on EP 450430; JP  
 3122153 B2 Previous Publ. JP 06339383; JP 3193917 B2 Previous Publ. JP  
 2001103988

PRAI DE 1990-4009676 19900326

REP NoSR.Pub; 6.Jnl.Ref; EP 238023; GB 2151635; JP 60199383; JP 61063291; US  
 4840903

IC C07H021-04; C07K015-04; C12C011-00; C12N001-19; C12N009-02; C12N015-63;  
 C12P007-06; C12P019-34

ICM C12N001-19; C12N015-09; C12N015-53

ICS C07H021-04; C07K013-00; C07K015-04; C12C011-00; C12N001-14;  
 C12N001-21; C12N009-02; C12N009-04; C12N015-63; C12N015-81;  
 C12P007-06; C12P007-10; C12P019-34; C12P021-02

ICI C12N009-02; C12N009-02; C12N015-09; C12N015-09; C12N015-09; C12R001:645;  
 C12R001:84; C12R001:84; C12R001:85; C12R001:865; C12N001-19;  
 C12N001-19; C12N001-19; C12N001-21; C12N009-04; C12N015-09;  
 C12P007-06; C12P007-06; C12P007-06; C12P007-06; C12R001:01;  
 C12R001:01; C12R001:645; C12R001:645; C12R001:84; C12R001:84;  
 C12R001:84; C12R001:84; C12R001:865; C12R001:865; C12N001-19;  
 C12R001:865; C12N009-02; C12R001:865; C12P007-06; C12R001:865;  
 C12N015-53; C12R001:645; C12N001-19; C12R001:865; C12N009-02,  
 C12R001:865

AB DE 4009676 A UPAB: 19971030

New **DNA** sequence (I) comprises a structural **gene**  
 encoding a **xylose reductase** (XR) and/or xylyl  
 dehydrogenase (XDH) and is able to express the enzyme(s) in a  
 microorganism.

Also new are (1) combinations of (I) with other **DNA** halogen  
 sequences for regulating expression; (2) vectors and microorganisms containing  
 (I), and (3) XR and XDH produced by expressing (I).

More specifically, (I) is derived from a **yeast**,  
 specifically *Pichia stipitis* CBS 5773 (DSM 5855). The specification  
 includes sequences for **DNA** fragments which encode XR (2040  
 bases) and XDH (1950 bases), and the derived structures (318 and 363  
 amino acids, respectively).

USE/ADVANTAGE - XR and XDH are useful (1) for production of ethanol from  
 xylose (a waste prod. of cellulose mfr.); (2) for production of biomass and  
 (3) for recovery of NADP(+) for NADPH. The microorganisms transformed with  
 (I) can ferment highly concentrate carbohydrate solns. prior art and are  
 tolerant to EtOH, pH and temperature. Also contemplated is production of  
 specific

proteins (II) in *P. stipitis* by expressing the structural **gene**  
 for (II) under control of the 5'-regulatory region of the XR and XDH  
**genes** of *P. stipitis* (these are inducible by xylose) and/or the  
 ADH1 promoter of *S. cerevisiae* and/or the glucoamylase promoter of  
*Schwanniomyces occidentalis*. *P. Stipitis* has an efficient secretory  
 system and can use xylose as a C source. @ (50pp Dwg.No.0/7)

FS CPI

FA AB; DCN

MC CPI: B04-B02B2; B04-B02C2; B04-B04A1; D05-C03B; D05-H03B;  
 D05-H05; D05-H12; E10-E04E2

ABEQ EP 450430 A UPAB: 19931113

New **DNA** sequence (I) comprises a structural **gene** encoding a **xylose reductase** (XR) and/or xylyl dehydrogenase (XDH) and is able to express the enzyme(s) in a microorganism.

Also new are (1) combinations of (I) with other **DNA** halogen sequences for regulating expression; (2) vectors and microorganisms contg. (I), and (3) XR and XDH produced by expressing (I).

More specifically, (I) is derived from a **yeast**, specifically *Pichia stipitis* CBS 5773 (DSM 5855). The specification includes sequences for **DNA** fragments which encode XR (2040 bases) and XDH (1950 bases), and the derived structures (318 and 363 amino acids, respectively).

USE/ADVANTAGE - XR and XDH are useful (1) for prodn. of ethanol from xylose (a waste prod. of cellulose mfr.); (2) for prodn. of biomass and (3) for recovery of NADP(+) for NADPH. The microorganisms transformed with (I) can ferment highly conc. carbohydrate solns. prior art and are tolerant to EtOH, pH and temp.. Also contemplated is prodn. of specific proteins (II) in *P. stipitis* by expressing the structural **gene** for (II) under control of the 5'-regulatory region of the XR and XDH **genes** of *P. stipitis* (these are inducible by xylose) and/or the ADH1 promoter of *S. cerevisiae* and/or the glucoamylase promoter of *Schwanniomyces occidentalis*. *P. Stipitis* has an efficient secretory system and can use xylose as a C source. @ (50pp Dwg.No.0/7)

ABEQ DE 4009676 C UPAB: 19931122

Recombinant **DNA** sequence that encodes the prodn. of an xylosereductase and/or xylitoldehydrogenase has been utilised in expression vectors contg. this **DNA** to produce the enzymes. Host cells have been transformed with these vectors and then propagated to produce the exogenous polypeptides. The **nucleotide** sequence of the **cdNA** and the aminoacid sequences of the polypeptides are defined.

USE - The prods. facilitate the degradation of xylose from wood pulp, leading to the conversion of waste biomass to alcohol.  
Dwg.0/7

ABEQ EP 450430 B UPAB: 19970723

New **DNA** sequence (I) comprises a structural **gene** encoding a **xylose reductase** (XR) and/or xylyl dehydrogenase (XDH) and is able to express the enzyme(s) in a microorganism.

L66 ANSWER 11 OF 11 WPIX COPYRIGHT 2004 THOMSON DERWENT on STN

AN 1990-276784 [37] WPIX

DNN N1990-213906 DNC C1990-119559

TI **DNA** coding for placenta-specific protein-9 - and recombinant protein with **aldose reductase** activity.

DC B04 D16 P34 S03

IN GRUNDMANN, U; AMANN, E

PA (BEHW) BEHRINGWERKE AG

CYC 18

PI EP 386733 A 19900912 (199037)\*

R: AT BE CH DE ES FR GB IT LI LU NL SE

DE 3907744 A 19900920 (199039)

AU 9051103 A 19900913 (199044)

PT 93381 A 19901107 (199047)

CA 2011877 A 19900910 (199048)

JP 02295486 A 19901206 (199104)

EP 386733 B1 19950705 (199531) DE 11p C12N015-12

R: AT BE CH DE DK ES FR GB IT LI LU NL SE

DE 59009360 G 19950810 (199537) C12N015-12

ES 2076238 T3 19951101 (199550) C12N015-12

IE 67797 B 19960501 (199629) C12N015-12

ADT EP 386733 A EP 1990-104352 19900307; DE 3907744 A DE 1989-3907744

19890310; JP 02295486 A JP 1990-59800 19900309; EP 386733 B1 EP

1990-104352 19900307; DE 59009360 G DE 1990-509360 19900307, EP  
 1990-104352 19900307; ES 2076238 T3 EP 1990-104352 19900307; IE 67797 B IE  
 1990-853 19900309

FDT DE 59009360 G Based on EP 386733; ES 2076238 T3 Based on EP 386733

PRAI DE 1989-3907744 19890310

REP 1.Jnl.Ref; EP 37963; 01Jnl.Ref

IC A61K031-70; A61K037-02; A61N037-02; C07H021-04; C07K013-00; C07K015-12;  
 C07K015-28; C12N001-21; C12N005-00; C12N015-12; C12P021-02; C12Q001-68;  
 G01N033-53; G01N033-68  
 ICM C12N015-12  
 ICS A61K031-70; A61K037-02; A61N037-02; C07H021-04; C07K013-00;  
 C07K015-12; C07K015-28; C12N001-21; C12N005-00; C12P021-02;  
 C12Q001-68; G01N033-53; G01N033-577; G01N033-68

ICI C12N001-21, C12R001:

AB EP 386733 A UPAB: 19930928  
 The following are claimed: (a) **DNA** coding for placenta-specific protein 9 (PP9), where the amino acid sequence of PP9 and the coding sequence of the **DNA** are shown in the fig.; (b) **DNA** and RNA which hybridise with **DNA** (a) under stringent conditions; (c) **gene** structures, vectors and transformed cells containing **nucleic acids** (a) or (b); (d) PP) when produced in *E. coli*, **yeast** or animal cells by expression of **DNA** (a); (e) polyclonal and monoclonal antibodies specific to PP9, when produced by immunisation with recombinant  
 USE - PP9 is probably identical to human **aldose reductase** and is thus useful for screening and identifying **aldose reductase** inhibitors for treatment of diabetic complications. The **nucleic acid** and antibodies are useful for diagnostic purposes, and the antibodies are also useful for purification of PP9 by affinity chromatography.  
 1/1

FS CPI EPI GMPI

FA AB; GI

MC CPI: B04-B02B1; B04-B02B2; B04-B02C2; B04-B04A; B04-B04C5; B04-B04C6;  
 B12-H05; D05-H09; D05-H11; D05-H12  
 EPI: S03-E14H

ABEQ EP 386733 B UPAB: 19950810  
 A **nucleotide** sequence shown in Table 1, or a sequence derived therefrom on the basis of the degeneracy of the **genetic code**, coding for placenta-specific protein PP9.  
 Dwg.0/1

=> d his

(FILE 'HOME' ENTERED AT 15:35:08 ON 04 MAR 2004)

FILE 'REGISTRY' ENTERED AT 15:35:42 ON 04 MAR 2004

SET COST OFF

E XYLOSE REDUCTASE/CN

|    |                            |
|----|----------------------------|
| L1 | 4 S E3                     |
|    | E XYLITOL DEHYDROGENASE/CN |
| L2 | 2 S E3                     |
|    | E XYLULOKINASE/CN          |
| L3 | 1 S E3                     |
| L4 | 26 S XYLOSE REDUCTASE      |
| L5 | 7 S XYLITOL DEHYDROGENASE  |
| L6 | 33 S XYLULOKINASE          |

FILE 'HCAPLUS' ENTERED AT 15:37:10 ON 04 MAR 2004

|    |   |
|----|---|
| L7 | 2967 S L1-L6  |
| L8 | 464 S XYLOSE REDUCTASE OR XYLITOL DEHYDROGENASE OR XYLULOKINASE |
| L9 | 3153 S ALDOSE REDUCTASE   |

L10 68 S XYLULOSE REDUCTASE  
 L11 50 S XYLULOSE KINASE  
 L12 3760 S L7-L11  
 L13 218 S L12 AND YEAST  
 E YEAST/CT  
 L14 25 S L12 AND E3-E53  
 E E53+ALL  
 L15 12225 S E1  
 E E2+ALL  
 L16 34588 S E6,E5+NT  
 L17 25 S L12 AND L15,L16  
 L18 218 S L13,L14,L17  
 L19 1 S YEAST(L) 1400 (L) LNH(L) ST  
 E SACCHAROMYCES/CT  
 L20 9 S L12 AND E3  
 L21 114 S L12 AND E3-E196  
 E E3+ALL  
 L22 0 S L12 AND E4  
 L23 113 S L12 AND E5+NT  
 L24 269 S L18,L20-L23  
 L25 32 S L24 AND DNA  
 L26 31 S L24 AND PLASMID  
 L27 20 S L24 AND CHROMOSOM?  
 L28 126 S L24 AND GENE  
 L29 74 S L24 AND GENETIC?/SC,SX  
 L30 130 S L25-L29  
 L31 269 S L24-L30  
 E WO97-US7663/AP,PRN  
 L32 1 S E3,E4  
 E US96-016865/AP,PRN  
 L33 1 S E5  
 E HO N/AU  
 L34 20 S E3,E11,E12  
 L35 36 S E28,E31,E32  
 E CHEN Z/AU  
 L36 722 S E3,E7  
 E CHEN ZHENG/AU  
 L37 261 S E3,E4  
 L38 8 S E51  
 L39 1 S L31 AND L32,L33  
 L40 11 S L31 AND L34-L38  
 L41 11 S L32,L33,L39,L40  
 L42 134 S L31 AND (PD<=19960506 OR PRD<=19960506 OR AD<=19960506)  
 L43 9 S L41 AND L42  
 L44 11 S L41,L43  
 L45 27 S L42 AND GENETIC?/SC,SX  
 L46 31 S L44,L45  
 L47 105 S L42 NOT L46  
 SEL DN AN 22 34 L47  
 L48 2 S E1-E6 AND L47  
 L49 33 S L46,L48 AND L7-L48  
 SEL HIT RN

FILE 'REGISTRY' ENTERED AT 16:16:43 ON 04 MAR 2004

L50 14 S E7-E20

L51 14 S L50 AND L1-L6

FILE 'REGISTRY' ENTERED AT 16:17:14 ON 04 MAR 2004

FILE 'HCAPLUS' ENTERED AT 16:17:29 ON 04 MAR 2004

FILE 'WPIX' ENTERED AT 16:17:48 ON 04 MAR 2004

L52 784 S L8/BIX OR L9/BIX OR L10/BIX

L53 24 S L52 AND YEAST/BIX  
L54 0 S L19/BIX  
L55 11 S L52 AND SACCHAROMYC?/BIX  
L56 21 S L52 AND (?PLASMID? OR ?CHROMOSOM?)/BIX  
L57 38 S L53,L55,L56  
L58 2 S L52 AND (HO N? OR CHEN Z?)/AU  
L59 2 S L57 AND L58  
L60 27 S L57 AND D05-H?/MC  
L61 30 S L57 AND (GENE OR GENETIC? OR DNA OR CDNA)/BIX  
L62 15 S L57 AND (?NUCLEIC? OR ?NUCLEO?)/BIX  
L63 32 S L59-L62  
L64 6 S L57 NOT L63  
SEL DN AN 5 15-17 20 25 27-31 L63  
L65 11 S E21-E43 AND L63  
L66 11 S L59,L65

FILE 'WPIX' ENTERED AT 16:25:58 ON 04 MAR 2004

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